```
synw(deactivating,n).
synw(deactivating, ving).
synw(deactivation,n).
synw(death,n).
synw(demethylate, v).
synw(demethylate, vp).
synw(demethylated, ved).
synw (demethylated, ven).
synw(demethylates, vp).
synw(demethylating,n).
synw (demethylating, ving).
synw(demethylation, n).
synw(dephosphorylate, v).
synw(dephosphorylate, vp).
synw(dephosphorylated, ved).
synw(dephosphorylated, ven).
synw(dephosphorylates, vp).
synw(dephosphorylating, n).
synw(dephosphorylating, ving).
synw(dephosphorylation, n).
synw(die,v).
synw(die,vp).
synw(died, ved).
synw(died, ven).
synw(dies, vp).
synw(disassemble, v).
synw(disassemble, vp).
synw(disassembled, ved).
synw(disassembled, ven).
synw(disassembles, vp).
synw(disassembling, n).
synw(disassembling, ving).
synw(disassembly, n).
synw(discharge, n).
synw(discharge, v).
synw(discharge, vp).
synw(discharged, ved):
synw(discharged, ven).
synw(discharges, vp).
synw(discharging,n).
synw(discharging, ving).
synw(disengage, v).
synw(disengage, vp).
```

```
synw(constrain, vp).
synw(constrained, ved).
synw(constrained, ven).
synw(constraining,n).
synw(constraining, ving).
synw(constrains, vp).
synw(constraint,n).
synw(coprecipitate, v).
synw(coprecipitate, vp).
synw(coprecipitated, ved).
synw(coprecipitated, ven).
synw(coprecipitates, vp).
synw(coprecipitating,n).
synw(coprecipitating, ving).
synw(coprecipitation ,n).
synw(copurification ,n).
synw(copurified , ved).
synw(copurified , ven).
synw(copurifies, vp).
synw(copurify, vp).
synw(copurify,v).
synw(copurifying ,n).
synw(copurifying , ving).
synw(couple , vp).
synw(couple, v).
synw(coupled, ved).
synw(coupled, ven).
synw(couples, vp).
synw(coupling,n).
synw(coupling, ving).
synw(cut,n).
synw(cut, v).
synw(cut, ved).
synw(cut, ven).
synw(cut, vp).
synw(cuts, vp).
synw(cutting,n).
synw(cutting, ving).
synw(deactivate, v).
synw(deactivate, vp).
synw(deactivated, ved).
synw(deactivated, ven).
synw(deactivates, vp) .
```

```
synw(causing, n).
synw(causing, ving).
synw(cleavage,n).
synw(cleave, v).
synw(cleave, vp).
synw(cleaved, ved).
synw(cleaved, ven).
synw(cleaves, vp).
synw(cleaving,n).
synw(cleaving, ving).
synw(coimmunoprecipitate, v).
synw(coimmunoprecipitate, vp).
synw(coimmunoprecipitated, ved).
synw(coimmunoprecipitated , ven).
synw(coimmunoprecipitates, vp).
synw(coimmunoprecipitating ,n).
synw(coimmunoprecipitating , ving).
synw(coimmunoprecipitation ,n).
synw(combination ,n).
synw(combine , v).
synw(combine , vp).
synw(combined , ved).
synw(combined , ven).
synw(combines, vp).
synw(combining ,n).
synw(combining , ving).
synw(conjugate , v).
synw(conjugate , vp).
synw(conjugated , ve).
synw(conjugated , ved).
synw(conjugates, vp).
synw(conjugating ,n).
synw(conjugating , ving).
synw(conjugation ,n).
synw(connect , vp).
synw(connect, v).
synw(connected , ve) . - -
synw(connected , ved).
synw(connecting ,n).
synw(connecting , ving).
synw(connection ,n).
synw(connects, vp).
synw(constrain, v).
```

```
synw(attached , ven).
synw(attaches, vp).
synw(attaching ,n).
synw(attaching , ving).
synw(attachment,n).
synw(bind, v).
synw(bind, vp).
synw(binding, n).
synw(binding, ving).
synw(binds, vp).
synw(block, v).
synw(block, vp).
synw(blockage,n).
synw(blocked, ved).
synw(blocked, ven).
synw(blocking,n).
synw(blocking, ving).
synw(blocks, vp).
synw(bound, ved).
synw(bound, ven).
synw(break, v).
synw(break, vp).
synw(breakage, n).
synw(breaking, n).
synw(breaking, ving).
synw(breaks, vp).
synw(broke, ved).
synw(broken, ven).
synw(catalyzation,n).
synw(catalyze,v).
synw(catalyze, vp).
synw(catalyzed, ved).
synw(catalyzed, ven).
synw(catalyzes, vp).
synw(catalyzing,n).
synw(catalyzing, ving).
synw(causation,n).
synw(cause,n).
synw(cause, v).
synw(cause, ven).
synw(cause, vp).
synw(caused, ved).
synw(causes, vp).
```

```
synw(activate, vp).
synw(activated, ved).
synw(activated, ven).
synw(activates, vp).
synw(activating,n).
synw(activating, ving).
synw(activation, n).
synw(add, v).
synw(add, vp).
synw(added, ved).
synw(added, ven).
synw(adding,n).
synw(adding, ving).
synw(addition,n).
synw(adds, vp).
synw(after, prep).
synw(aggregate , v).
synw(aggregate , vp).
synw(aggregated , ved).
synw(aggregated , ven).
synw(aggregates, vp).
synw(aggregating ,n).
synw(aggregating , ving).
synw(aggregation ,n).
synw(arrest, n).
synw(arrest, v).
synw(arrest, vp).
synw(arrested, ved).
synw(arrested, ven).
synw(arresting, n).
synw(arresting, ving).
synw(arrests, vp).
synw(associate, v).
synw(associate, vp).
synw(associated, ved).
synw(associated, ven).
synw(associates, vp).
synw(associating,n).
synw(associating, ving).
synw(association, n).
synw(attach , v).
synw(attach, vp).
synw(attached , ved).
```

```
synp(set, [set, free], vp).
synp(sets, [sets, free], vp).
synp(sets, [sets, free], vp).
synp(setting, [setting, free],n).
symp(setting, [setting, free],n).
symp(setting, [setting, free], ving).
symp(setting, [setting, free], ving).
synp(suppress, [suppress, activity, of], v).
synp(suppress, [suppress, activity, of], vp).
symp(suppressed, [suppressed, activity, of], ved).
symp(suppressed, [suppressed, activity, of], ven).
synp(suppresses, [suppresses, activity, of], vp).
synp(suppressing, [suppressing, activity, of],n).
synp(suppressing, [suppressing, activity, of], ving).
synp(suppression, [suppression, of, activity, of], n).
synp(switch, [switch, on, the, activity, of], vp).
synp(switched,[switched, on, the, activity, of], ved).
synp(switched,[switched, on, the, activity, of], ved).
synp(switched, [switched, on, the, activity, of], ved).
synp(switched, [switched, on, the, activity, of], ved).
synp(switched,[switched, on, the, activity, of], ved).
synp(switches, [switches, on, the, activity, of], vp).
synp(up,[up,'-',regulate],v). % A up-regulates B B --> A
synp(up, [up, '-', regulate], vp). % A up-regulates B B --> A
synp(up,[up,'-',regulated], ved).
synp(up, [up, '-', regulated], ven). % A up-regulates B B --> A
symp(up, [up, '-', regulates], vp).
symp(up, [up, '-', regulating], n). % A up-regulates B B --> A
synp(up, [up, '-', regulating], ving). % A up-regulates B B --> A
symp(up, [up, '-', regulation], n).
synp(was, [was,a,means,of, producing], ved).
symp(was, [was,due,to],ved).
synp(were, [were,a,means,of, producing],ved). % ?
synp(were, [were, due, to], ved).
synw(acetylate, v).
synw(acetylate, vp).
synw(acetylated, ved).
synw(acetylated, ven).
synw(acetylates, vp).
synw(acetylating,n).
synw(acetylating, ving).
synw(acetylation,n).
synw(activate, v).
```

```
synp(n,[n,'-',glycosylates],vp).
symp(n,[n,'-',glycosylating],n).
synp(n,[n,'-',glycosylating],ving).
synp(n,[n,'-',glycosylation],n).
synp(n, [n, '-', terminal, proteolysis], n).
synp(o,[o,'-',glycosylate],v).
synp(o, [o, '-',glycosylate], vp).
synp(o, [o, '-', glycosylated], ved).
synp(o, [o,'-',glycosylated],ven).
synp(o,[o,'-',glycosylates],vp).
synp(o,[o,'-',glycosylating],n).
synp(o,[o,'-',glycosylating],ving).
synp(o, [o, '-', glycosylation], n).
symp(only, [only, after], prep).
synp(prolyl, [prolyl,'-',4,'-',hydroxylate],v ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylate],vp).
synp(prolyl, [prolyl,'-',4,'-',hydroxylated],ved ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylated],ven ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylates],vp).
synp(prolyl, [prolyl,'-',4,'-',hydroxylating],n ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylating],ving ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylation],n).
synp(result, [result, from], v).
synp(result, [result, from], vp).
synp(result, [result, in], v).
synp(result, [result, in], vp).
symp(resulted, [resulted, from], ved).
synp(resulted, [resulted, from], ven).
synp(resulted, [resulted, in], ved).
synp(resulted, [resulted, in], ven).
symp(resulting, [resulting, from], n).
symp(resulting, [resulting, from], ving).
symp(resulting, [resulting,in],n).
synp(resulting,[resulting,in],ving).
symp(results, [results, from], vp).
synp(results,[results,in],vp).
symp(set, [set, free], v).
symp(set, [set, free], v).
symp(set, [set, free], ved).
symp(set, [set, free], ved).
symp(set, [set, free], ven).
synp(set, [set, free], ven).
symp(set, [set, free], vp).
```

```
synp(having, [having, an, active, role, in], n).
synp(having, [having, an, active, role, in], ving).
symp(is, [is,a,means,of, producing],vp).
synp(is, [is,due,to],vp).
synp(functions,[functions,as,a,negative,regulator,of],vp).
synp(function, [function, as, a, negative, regulator, of], vp).
symp(lead, [lead, to], v).
symp(leads, [leads,to],vp).
symp(leading, [leading, to], n).
synp(leading, [leading, to], ving ).
symp(leads, [leads, to], vp).
synp(led, [led, to], ved).
synp(led, [led, to], ven).
synp(may,[may,be,responsible,for],vp).
synp(mediate, [mediate, a, signal], v).
                                            %A mediates a signal to
synp(mediate, [mediate, a, signal], vp).
synp(mediated, [mediated, a, signal], ved).
synp(mediated,[mediated, a, signal], ven).
synp(mediates, [mediates, a, signal], vp).
synp (mediating, [mediating, a, signal], n).
synp (mediating, [mediating, a, signal], ving).
synp(mediation, [mediation, of, a, signal], n).
synp(n,[n,'-',acetylate],v).
synp(n,[n,'-',acetylate],vp).
synp(n, [n, '-', acetylated], ved).
synp(n,[n,'-',acetylated],ven).
synp(n, [n, '-', acetylates], vp).
synp(n, [n, '-', acetylating], n).
synp(n,[n,'-',acetylating],ving).
synp(n,[n,'-',acetylation],n).
synp(n,[n,'-',acylate],v).
symp(n, [n, '-', acylate], vp).
symp(n, [n, '-', acylated], ved).
synp(n,[n,'-',acylated],ven).
synp(n,[n,'-',acylates],vp).
synp(n,[n,'-',acylating],n).
synp(n,[n,'-',acylating],ving).
synp(n,[n,'-',acylation],n).
synp(n, [n, '-', glycosylate], v).
synp(n, (n, '-', glycosylate], vp).
synp(n,[n,'-',glycosylated],ved).
synp(n, [n, '-', glycosylated], ven).
```

Page 3

```
symp(being, [being, due, to], n).
synp(being, [being, due, to], ving).
synp(caused, [caused, by], ved).
synp(caused, [caused,by],ven).
symp(convey, [convey, a, signal], v).
synp(convey, [convey, a, signal], vp).
synp(conveyed, [conveyed, a, signal], ved).
synp(conveyed,[conveyed,a, signal],ven).
synp(conveying,[conveying, a, signal], ving).
symp(conveying, [conveying, a, signal], n).
synp(conveys,[conveys,a, signal],vp).
symp(dissociate, [dissociate, from], vp).
synp (dissociate, [dissociate, from], v).
synp (dissociated, [dissociated, from], ved).
symp (dissociated, [dissociated, from], ven).
symp(dissociates, [dissociates, from], vp).
symp(dissociating, [dissociating, from], n).
synp(dissociating,[dissociating,from],ving).
symp(dissociation, [dissociation, from], n).
synp(down, [down, '-', regulate], v).
Α
synp(down, [down, '-', regulated], ved).
synp(down, [down, '-', regulated], ven).
synp(down, [down, '-', regulates], vp).
synp(down, [down, '-', regulating], n).
synp(down, [down, '-', regulating], ving).
synp(down, [down, '-', regulation], n).
synp(due,[due,to,the,fact,that],adj).
synp(due,[due,to],adj). % ?
symp(form, [form, complex], v).
symp(form, [form, complex], vp).
symp(formation, [formation, of, complex], n).
symp(formed, [formed, complex], ved).
symp(formed, [formed, complex], ven).
synp(forming,[forming, complex],n).
synp(forming, [forming, complex], ving).
symp(forms, [forms, complex], vp).
symp(had, [had,an,active,role,in],ved).
synp(had, [had, an, active, role, in], ven).
symp(has, [has,an,active,role,in],vp).
symp(have, [have, an, active, role, in], v).
symp(have, [have, an, active, role, in], vp).
```

```
% lexsyn.pat
% revised March 17, 2000
                 SYNTACTIC LEXICON FOR ACTIONS
% Contains syntactic entries for action type words and phrases
% synp(+Wordl,+Wordlist,+Syn)
% synp: Wordl is first word of phrase, Wordlist is list of words i
n phrase
% synp: Syn is syntactic categorey
% synw(+Word,+Syn) is same as synp except there is no wordlist
synp(account, [account, for], v).
synp (account, [account, for], vp).
symp(accounted, [accounted, for], ved).
symp(accounted, [accounted, for], ven).
symp(accounting, [accounting, for], ving).
symp(accounting, [accounting, for], n).
synp(accounts, [accounts, for], vp).
synp(add, [add, up], vp).
symp(add, [add, up], v).
synp(added, [added, up], ved).
synp(added, [added, up], ven).
synp(adding,[adding, up],n).
synp(adding, [adding, up], ving).
synp(adds, [adds, up], vp).
symp(am, [am,a,means,of, producing],vp).
synp(am, [am,due,to],vp).
synp(are, [are,a,means,of, producing],vp).
symp(are, [are,due,to],vp).
synp(as,[as,a,result,of],prep).
symp(attributable, [attributable, to], vp). % ?
synp(attributed, [attributed, to], ven).
synp(based, [based, on], ven).
synp(based, [based, upon], ven).
synp(be, [be,a,means,of, producing],v).
symp(be, [be,due,to],v).
synp(because,[because,of],prep).
symp(been, [been, a, means, of, producing], ven).
synp(been, [been, due, to], ven).
synp(being, [being,a,means,of, producing],n).
synp(being, [being, a, means, of, producing], ving).
```

Appendix B Page 1

```
wdef(pkc,protein, 'protein kinase C').
wdef(position, site, site).
wdef(positions, site, site).
wdef(protease, protein, protease).
wdef(ps1,protein,'presenilin 1').
wdef(ps2,protein,'presenilin 2').
wdef(rap1, protein, 'Rap1').
wdef(ras, protein, 'Ras').
wdef(receptors, substance, receptor).
wdef(rela, protein, 'RelA').
wdef (residues, substance, residue).
wdef(responsive, state, active).
wdef(s6, protein, 'S6').
wdef(selectively, constraint, selective).
wdef(ser112, site, 'Ser112').
wdef(ser136, site, 'Ser136').
wdef(ser32, smallmolecule, 'Ser32').
phrase(ps1, protein
wdef(ser36, smallmolecule, 'Ser36').
phrase(ps1, protein, [ps1,'-',ctf], 'ps1-ctf',r).
wdef(sh2,domain, 'SH2').
wdef(sh3,domain,'SH3').
wdef(shc, protein, 'Shc').
wdef(signalsome, complex, signalsome).
wdef(sites, site, site).
wdef(sos, protein, 'Sos').
wdef(staurosporine, smallmolecule, staurosporine).
wdef(sts,smallmolecule,'STS').
wdef(tcr, complex, 'T-cell receptor').
wdef(tetracycline, smallmolecule,tetracycline).
wdef(thr229, aminoacid, 'Thr229').
wdef(thr308, aminoacid, 'Thr308').
wdef(thr389, aminoacid, 'Thr389').
wdef (threonine, aminoacid, threonine).
wdef(tyrosine, aminoacid, tyrosine).
wdef (unresponsive, state, inactive).
wdef(unstimulated, state, inactive).
wdef(zvad, smallmolecule, 'zVAD').
```

-112	- 97		-112	-97		-112	- 97		-112	-97		-112	- 97		-112	-97		-112	-97		-112	- 97		-112	-97		-112	- 97		-112	-97		-112	•	
-270	-255		743	-255		-270	-255		-270	-255		-270	-255		-270	-255		-270	-255		.270	-255		- 270	-255		-270	-255		-270	-255		-270	•	
-27	-12		-27	-12		-27	-12		-27	-12		193	-12		-27	-12		-27	-12		.27	.12		-27	-12		-27	-15		-27	-12		-27	•	
11	27		11.	27		11	72		11	27		11	27		253	27		11	27		11	27		11	27		11	27		11	27		11	*	
-69	- 54		- 69	-54		-69	-54		-69	-54		-69	-54		69-	-54		-69	-54		69.	-54		-69	.54		-69	, 54		-69	, 54		-69	•	
-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	•	
. 88	-73		-88	-73		-88	-73		-88	- 73		-88	-73		-88	-73		- 88	-73		- 88	-73		- 88	- 73		-88	-73		-88	-73		· 8 B	•	
25	41		25	41		25	41		25	41		25	41		25	41		25	41		25	41		25	41		301	41		25	41		25	•	
-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	•	
94	-677		-692	-677		-692	-677		-692	-677		-692	-677		-692	-617		-695	-677		-692	-677		-695	-677		-695	-677		-692	-677		-692	•	
-146	-130		-146	-130		-146	-130		-146	-130		-146	-130		-146	-130		25	-130		-146	-130		-146	-130		-146	-130		-146	-130		-146	*	
423	438	•	423	438	*	423	438	*	423	438	٠	423	438	•	423	438	•	423	438	•	423	438	*	423	438	•	423	438	*	423	438	•	423	•	0
-651	-635	*	-651	-635	•	-651	-635	*	-284	-635	٠	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	*	-651	•	•
570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	588	- 782	570	585	-782	570	585	-782	570	585	-782	968	•	•
357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	468	372	-1256	357	•	•
	-36																																	•	•
-367	-352	-732	-367	-352	-732	- 86	-352	- 732	-367	-352	- 732	-367	-352	-732	-367	-352	-732	-367	-352	-732	- 86	-352	-732	-367	-352	-732	-367	-352	-732.	-367	-352	-732	-367	•	•
-194	-178	-6731	-194	.178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-88	-178	-6731	-194	٠	*
964	979	-5731	964	979	-5731	964	979	-5731	964	979	-5731	964	979	-5731	964	979	-5731	964	979	-5731	964	979	-5731	1364	979	-5731	964	979	-5731	964	919	.5731	964	•	•
191	206	-41	191	206	-41	191	206	-41	191	506	-41	191	206	-41	191	506	-41	191	206	-41	191	206	-41	191	206	-41	191	206	-41	191	902	-41	191	•	•
10	•	ı	11	•	•	12	٠	•	13	•	•	14	٠	٠	15	•	ť	16	•	•	11	٠	,	18	,	•	19	,		20	,	,	21	1	•

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- 130		-1251	-130		-2517	-130		-1646	-130		- 85	-130		-1870	-130		-1461	-130		-1040	-130		-2147	-130		-994	-130		-68	-130		-1315	-130		249	-131		-394	*	
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372	-3334	864	372	-3649	1320	372	-5023	1802	372	-5903	-62	372	-6067	86	372	-6147	-3062	372	-6229	-2076	372	-6317	-3099	372	-6443	-1083	372	-5625	-3003	372	-6737	-2024	372	-7041	-1381	371	-5989	-1054	•	•
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•			•	. 964	585	-156	- 964	583	.156	. 964	5.65	-311	-1026	585	-419	1001	585	.403	-1071	585	-245	.1090	585	-427	869	585	.172	1365	585	-257	1272	585	.245	1677	 	198.	585	-173	-213	585	. 264	-963	585	.153	- 963	585	-203	1629	585	. 351
.2538	1104	172	.3256	1177	372	3285	.1177	372	-3285	.1177	374	-2365	-1239	372	. 1988	-19	372	•	2		•					372	,		372	-2615	.1041	372	-2681	544	372	26027	372	-3149	-1120	372	-2582	663	372	-3317	415	372	-2931	.1123	372	-2176
-1329	6S+-	.35	-1329	345	- 36	.1329	951	. 36	-1329	-1585	. 36	.5145	-1647	- 36	.1329	-1712	-36	-1329	-1692	-36	-1329	1156	.36	-1329	524	- 36	-1329	2224	- 36	-1329	640	.36	.1329	1034	.36	6751.	36.	-1329	2320	-36	-1329	1002	- 36	-1329	-1584	. 36	.1329	1423	96.	-1329
- 732	1840	-352	-732	326	-325	-732	-338	.352	-732	- 1901	-353	-41	-936	.325	- 732	-471	.352	-732	-2008	-352	-732	-2028	.352	.732	-1635	.352	- 732	- 805	-352	.732	-1765	-352	-732	527	-352	767.	-352	-732	-1845	-352	-732	322	-352	.732	335	-352	-732	69.	. 352	.732
-4780																																																		
9443	. 587	919	9458	.570	979	. 9432	1192	976	. 9432	.570	979	-106	.632	919	9519	969.	979	6096	1414	979	. 9583	290	919	6096	- 304	979	9012	-345	979	- 9073	1592	919	- 9209	-437	979	1175	979	- 9294	-513	979	- 9317	- 569	979	-9397	979	979	-9397	395	62.6	* * * * * * * * * * * * * * * * * * *
5.5	1360	205	-27	430	206	7	.1343	206	•	.102	206	-3832	2254	205	-30	. 556	206	118	.1450	206	~	163	206	695	256	206	9	. 242	206	- 4	.40	206	- 95	369	206	. 150	206	E.	-405	506	٠	-218	206	ŗ	-1342	206	٠.	1210	506	ŗ-
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6.		986	.97	308.	-97		-1916	-97		916	-97	;	2 6		.1741	-97		-1707	-97		555	ćó		202	9.5		17.16		-1732	-97		9997	, ,	-1588	-97		-1609	-97	,	-1633	5	1631			-1652	- 97
.255		-2104	-255	. 2161	-255		-2075	-255		-2005	-255	0	5007-	66.3	-1899	-255		-1865	-255		1436	255		185	255	1000	6297.		.1890	-255	,	C 607 -	667-	-1746	-255		-1767	-255		16/1-	667-	1021	. 255	1	-1810	-255
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7.7		-1822	27	.705	27		-646	27		686	27	ć		•	-1194	27		-1418	27		539	2.3		-13	27	01.7	2 6	i	84	27	į	101		493	27		393	27		010	7	.17	27	,	-871	27
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-635	•	-543	.635	-680	-635	•	-292	. 635	• (- 2385		-2385	-635	•	-2280	-635	•	-2245	-635	•	-2301	ςξη.	. ני	6/77-	. 650	-162	-635	•	-2271	-635	-1294	-635	•	-2126	-635	• ;	785-		45.6	-635	•	-2172	-635	•	.988	-635
585	.345		585	1321	585	-388	-1235	585	-276	2911.	969	923	585	-227	1348	585	-181	- 28	282	-329	. 243	200	687.	1040	-181	-1055	585	.396	-1050	585	1005	585	-165	906-	282	. 186	176-	282	- 952	585	-151	- 952	585	-272	016-	585
372	.2231	7741.	1225	-1534	372	-2084	-1448	372	-2523	67.51-	2760	.1074	372	-2780	968.	372	-3085	.1238	2/5	2622-	-1293	2/5	6706-	0077-	.3086	-1268	372	.2058	.1263	372	-1218	372	-3212	-1119	372	3048	0511.	2743	1164	372	3327	1164	372	2543	1183	372
.36	-1329	- 1885	- 1329	-1942	- 36	-1329	- 18	-36	-1329	99/1-	96.	-1786	.36	-1329	-646	- 36	-1329	1246	9 9	-1329	-1/01	95.	יבנו-	550	1329	604	- 36	.1329	1671	- 36	1526	-36	1329	1527	- 36	1329	00.	1329	1297	-36	1329	3011	-36	1329 .	1591	-36
-352	. 975	1077	.732	220	352	-732	1997	- 352	- 732	מות.	266-			.732	2303	-352	-732	-1345	765.	26/-	.2017	200	20'.	200	-732	.1992	-352	. 732	2245	.352	2111	.352	-732	1843	. 352 - cre	. 25/-	0471	.732			- 732 -	-612	.352	- 732 -	163 -	352
.178	2115	3707.	-6368	-472	-178	3724	1998	.178	1995	1761	10710	.1928	-178	3399	1823	-178	-4919	.1788	9,7,	21601	1844	2762	מ מ מ מ	. a.c.	09501	786	178	3830	. 954	-178	-604	-178	3436	1670	B/ 1-	1660		5835				1715		_	1734	m
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206		200	. 19	.285	206	-115	933	206		700		-737	205	.146	164	206	. 50	500	, c		200	2 0	2,43	206	, , ,	41	206	.107	.126	206	360	206	142 -	949	ָ פַּ		20.5	-28 -5	218	206	5. €-	363 -			-1350	
•	. 20.			136	•		137	• ,	, a.		•	139			140			141					143			144			145		146			147	•	148 .1		,	149 -1			150			151 -1	•

	.1772	16.	2501.	6797	ĥ.	-1826	.97		- 509	-97) C	À	-1857	76.		1451	-97		1512	.97	-	.616	. 97		700	'n	.10	-97		234	-97	;	7017-		-43	-97		1017.	, ,	-2167	6	•	-2167	- 97	
	1930	255	1004	P061.	ec.	-1984	. 255		-2015	- 255	3100	6107-	CC7.	-2015	-255		.2015	-255		-2015	.255			. 255		1 00	563	-2325	-255		-2325	-255	3000	-255	<u>.</u>	-2287	-255	1603	7007	667-	-2325	.255		-2325	-255	
	426	1,2	1231			-214	-12		-711	-12	456.	£0.	71.	-617	-12		-1067	-12		-419	-12		1358	15	0021.	277	3 4	117	.12		-1060	-12	-730	-12	!	207	-12	220		71.	115	.12		354	-12	
	483	3,1	150	5.	•	-939	27	į	06	21	644	, ,	N	-1734	27		-1734	27		-1734	2,		-1116	7.7	Ç	; ,	, -	-300	2.7		-1187	27	1 70	27		-437	27	151-	, ,	4	-277	27	-	-662	27	
	+80	. <u>S</u>	5.82		;	118	.54		1034	-54	נסנ	1 1	5	248	-54		243	-54		1041	.54		= ;	V		3.	;	217	-54		373	-54	-2124	-54		-705	54	. B.20		ζ.	-682	- 54		1963	-54	
	178	.335	-2064	.335	3	35	-335	:	1144	- 335	.573	3.5.		1026	-335		-224	-335		-854	-335	;	513	ردر. د	63	511	3	-30	.335		-2405	-335	.272	-335		-2367	- 135	131	7.5	3	2210	-335		87	-335	
	858	.73	-274	-73	•	-28	-73	;	-1145	5/-	105	5.	•	1125	-73		-971	ζ.	į	201	-73	;	קער נ	۲/۰	-1083	.73	!	-1033	-73		-1026	-73	392	-73		2350	٠/۶	-2143	. 7.	•	-2143	.73		-629	-73	
	983	4.2	-841	41		. 1689	41		07/1-	4	.122	. 4	:	-1720	41		-1720	4		-1720	4.	;	, ,	7	-2030	41	!	544	41		2206	41	2346	41		-1992	4	- 166	1.4	!	- 166	41		-493	41	
	1210	- 164	714	-164		1286	-164		780	*OT -	930	-164		314	-164		-174	- 164	;	532	-164		9671-	501	-469	-164		-2235	-164		-2235	-164	-2235	-164		941	50 T-	-658	-164		.1661	-164		2235	-164	
	.2352	. 677	767	-677		-2406	-677	į	C 5 0 .	/ / 0 -	145	-677		625	-677		-2437	-617		848	-677	6	2007		524	-617		-2747	.611		-745	-677	922	-677		2709		257	-677		. 2747	-617		2747	-677	
	-682	- 130	.929	-130		-216	-130		6,6,	05.7	890	-130		1289	-130		1229	-130	6	285	-130	ŕ	9 5	1	-338	-130		-770	-130		619	-130	-224	-130	!	- 298	271	1471	-130		420	.130		- 924	-130	
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•	2311	5.25	-466	-635	• ;	-210	٠ د و د	. 273	, <u>.</u>	•	489	-635	•	36	.635	•	1077	ر د و و ر		671.	-635	ā	5.63.5	•	-17	-635	•	-719	.635	•	151	٠ د د	.173	-635	• 6	9/1-	•	-777	-635	٠	992	-635	•	970	-635	
-258	0601	585	1083	585	.233	4-11-	מפט .	7711.	2 8 2	.258	1415	585	-258	-220	585	. 258	-1175	n 6	907.	0,11.	585	27.1.	283	.6830	-1485	585	-4293	.1485	585	-4293	1485	585 4293	.1485	585	.4293	6 8 8 6 8 8	-5089	454	585	-4293	-235	585	4293	.1485	585	2 4 2 4 5
. 261)	1303	2036	1357	372	.2745	7551.	275	328	372	-2613	-1388	372	-2613	-1388	372	.2613	-1388	2/5	\$10%	0,7.	372	98%	372	7	-444	372	- 76	-1698	372	- 76	-1698	376	-1698	372	. 76	372	4.	-631	372	- 16	1698	372	- 26	44.0	372	0
1329	1478	1329	76	-36	.1329	967	96.	128	.36	-1329	-1796	- 36	.1329	194	- 36	.1329	194	000	. 1367		95.	7	.36	-1329	66	-36	-1329	2370	-36	-1329	-174	-1329	1344	-36	-1329	36.	-1329	1019	-36	.1329	-183	-36	1329	842	96.	1323
732	1234	. 732	46	. 352	-732	1025	-732	274	- 352	.732	. 540	-352	.732	- 150	. 352	- 732	771	73.5	1059		732	1245	-352	.732	1901	- 352	-732	69	-352	.732	3/3	732	607	-352	-732	-352	-732	-576	-355	-732	- 790	-352	- 732	2422	755-	*****
1697	240	10569	-812	.178	.10641	27.	-10641	.122	.178	-10681	-1228	-178	10591	.1939	. 1.78	-10681	120	10401	720		10681	154	178	10681	800	178	111125	- 988	1.18	11125	0/01.	11125	-2249	178	.4918	-178	.11077	-2249	-178	-11125	66	. 178	-11125	182	1,4004.) ! ! !
. 5981	596	6956-	-750	979	.9641	0.0	. 9641	. 781	979	.9681	-781	919	.9581	. 781	979	.9581	2 0	. 96.81	787	. 0	. 9581	.781	626	- 9681	-1091	979	-10125				979				-10125	979	•	-1091		•	942			1601-		
977	1470	9.7	548			200					162										202											. ?		206	. 50.	206		69-			-798					
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-97		200	. 97		- 520	- 97	1650		;	-595	- 97		-1713	-97		-23	,	-1754	.6		.1813	Ló		1790	60		.1757	, ,	516	76,	,	1262	-97		291		-1825	-97		-1825	-97		-1825	-97	•	-1857	-97
-255		2776	252		1745	. 255	1808	.255		-1818	-255		-1811	-255		1861	557.	-1912	-255		1971	-255		1946	25.5		1915	567.	. 980	-255		-2015	-255		-2015	000	-1984	- 255		-1984	-255		-1984	-255		-2015	-255
12		505	2		-250	. 12	1566	27.	7.	280	-12		-350	-12		398	21-	- 169	.12		330	13		553	. 12		.1673	71.	707	-12	i	-445	-15	į	613	71.	-370	-12		928	-12		-654	-15		666	-12
7.13		823	2.1		.1463	27	124		ì	-1536	27		-128	27		551	7	.1014	27		591	27		519	27		. 1634	17	154	27	,	-1734	27	i	-1734	v	314	27		-1702	27		-1108	27	;	685	. 27
-54		101	75		624	-54	ā	2 4	5	-156	-54		594	-54		294	40	.122	-54		155	,54		-477	35.		-359	• > 4	690	5.5	;	-17	-54	ì	812	7	629	-54		868	- 54		723	- 54		35	-54
335		- 653	-335		-1825	-335	141	25.	7	-107	-335		-1952	-335		-1942	- 135	-247	-335		2.7	.335		.320	. 335		612	£ £ 5	121	.335	;	-1064	-335	:	-2095	000	-1359	-335		653	-335		485	-335	;	21	-335
-73		-1447	(۲۰		-480	.73	3631.		•	.14	-73		.1690	-73		.1679	- 73	-1099	-73		.1789	.73		987	-73		1129	٢).	1802	-73	1	-121	-73	,	27		246	-73		-297	- 73		-1802	-73		- 20 -	۲,
41		1334	41		1198	4	. 561	5	į	-1522	41		659	41		-874	~	1024	41		1466	41		20	41		34	4	.7.	41	!	-220	41	į	453	7	-1688	41		425	41	-	49	41	į	-1720	41
-164		-437	-164		170	.164	733	157	501	-1727	-164		962	-164		913	-164	. 131	-164		24	-164		823	-164		-1825	5 01.	.1891	-164		309	-164		-439	FOT-	1495	-164		-325	-164		287	-164	•	1653	-164
.677		-2051	.673		-2166	-617	0166-	7,77	9	-2240	-617		-2293	-677		-2283	-617	A.	-677		-2393	-677		1501	-677		875	//9-	- 2406	-677		-2437	-677	;	1562		-2405	-677		-2405	-677		123	-677	•	-2437	٠67.
.130		-1505	. 130		.752	.130	040		201	234	-130		23	-130		711	061.	~	.130		1762	-130		229	-130		1123	-130	5.24	130		~	-130	;	.331	251	- 992	-130		-545	-130		464	-130	;	20	.130
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-635	•	2010	.635	•	-146	.635	0010	5073	•	345	-635	•	-2252	-635	•	349	-635	. 291	-635	•	579	-635	•	-172	. 635	•	-2296	-63 5	910,	-635	•	237	-635	•	354	•	.513	-635	•	-259	-635	•	-1295	-635	• •	763	-635
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372	2451	1002	372	-2047	-1118	372	1101	372	-2340	-1191	372	-2379	-1245	372	-2599	-1235	372	-1285	372	-1585	-1344	372	-2785	898	372	-2904	.1288	7/5	-1901	372	-2143	919	372	-2613	-1388	215	-257	372	-2746	-1357	372	.2746	.493	372	-2140	-1388	372
.36	1329	1025	- 36	-1329	1219	-36	1329	26.	1329	.934	- 36	1329	1105	. 36	.1329	743	97.	.1691	.36	-1329	.1752	- 36	-1329	.1729	- 36	-1329	-1696	95	1329	-36	.1329	-1796	- 36	.1329	125	95.	133	-36	-1329	133	-36	-1329	156	. 36	-1329	403	.36
352	732	741	-352	.732	1942	.352	36/.	25.	. 732	1522	.352	-732	1386	-352	-732	-263	-352	1050	.352	-732	100	-352	732	267	.352	. 732	-1306	795.	1232	.352	.732	562	-352	.732	184	500.	1088	-352	- 732	.105	-352	-132	1571	-352	-732	436	-352
. 178	3915	725	178	4. 0.00 0.00	150	178	20201	96.1	-4242	10	-178	10409	101	178	-4885	558	.178	10.400	.178	4465	-1894	- 178	5484	265	178	5010	184	8/1-	4 t t O 1	-178	10641	.1939	.178	10681	573	ממט ל	1907	-178	6630	806	.178	10639	. 663	.178	66301	∵ ;	178
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2,00	7		1496	41		-1496	4.	1351	41		-97	41		970	4		- 52	4	1111		;	-1547	41		-1594	41.		-1533	4		191	41		- 410	:	-1617	41		393	41	,	325	43		- 833	41	1961	1951.
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1824	585	-176	89	585	.158	156.		-951	585	-414	1119	585	.379	-1105	585	-215	-1105	080	642	ָ מ ט ע	.189	1101	585	-311	-1050	585	-190	- 989	585	-330	-1047	585	y . 5 .	585	-215	- 94	585	-195	- 1000	585	-164	. 943	585	-148	1524	585	1083	2
.1226	372	.3124	-619	372	. 3267	-1164	3267	- 240	372	-2004	387	372	-2115	- 148	372	-2854	-1318	7/5	. 602	17.5	-3028	.1216	372	-2365	.1263	372	-3021	-1202	372	-2289	181	372	5112-	372	-2854	-1285	372	2984	.1213	372	.3215	-1156	372	.3355	276	372	£867.	2
. 1634	-36	1329	-1572	- 36	-1329	.1572	- 1329	-1572	-36	-1329	.1668	- 36	-1329	-1726	- 36	1329	1008	95.	5764	36.	-1329	.1624	- 36	-1329	-1671	- 36	-1329	.141	-36	-1329	-651	-36	6761-	98.	.1329	-110	-36	-1329	-1621	- 36	-1329	7.5B	- 36	-1329	-1417	-36	.1329	7 4
511	8 15	732	1683	352	. 732	. 1888	332	1 50	-352	.732	1984	-352	.732	372	.352	732	- 2042	200.	191		.732	1201	-352	-732	831	.352	.732	-328	-352	. 732	873	352	25/.	-352	-732	516	.352	-732	- 364	-352	-732	. 1365	-352	-732	1110	255-	25/-	.
154	178	4067	1183	-176	10361	0, 0	-1/8	1199	.178	-10361	606	-178	-10495	36	178	10579	653	B/ I -	1601	178	1206	.520	.178	10442	329	-178	-4118	628	-178	10415	-1810	-178	26401	-178	-4990	.173	-178	.3876	1290	-178	-4165	6001	-178	-2851	730	-178	10707	;
-619	626	.9453	.557	919	-9361	-557	. 9361	.557	979	-9361	-652															979	-9504	-595	919	-9415	179	979	. 4496	979	-9579	1292	979	-9537	1397	979	-9440	946	979	- 9353	-402	979	. 4017.	8 7 7
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	. 1945	667	-1945	-255		1586	-255		-1945	-255		-1891	-255	;	-1891	در۲ -	1991	-255		1681-	.255		19.45	255		1945	552		. 1945	667-	-1945	-255		-1945	567-	-1945	-255		-1945	-255		-1945	-255		
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	1496	<u>,</u>	156	- 54		-1744	-54		745	- 54		-382	-54	ļ	-872	٠. د	207	-54		317	. 54		648	5.4		.1744	.54		-311	, 04	-1290	.54		322	40,	-1744	- 54		-284	- 54		-1744	-54		
	219	C 8 6 :	-2025	-335		176	-335		-2025	-335		25	-338		.1971	4115	1,7	-335		-487	.335		332	-335		545	-335		664	crr.		-335		-134	crr.	109	-335		-583	-335		-214	-335		
	1763	?.	-1763	-73		283	-73		-1132	-73		66	.73		-174	٢/-	1,73	.73		-1709	- 73		-1763	.73		906	.73		351	?	686	-73		-1763	5/-	923	-73		-50	-73		9	٤٢٠		
	. 4 d 33	4	.395	41		-	41		-1649	4		-1596	41		-1596	4.1	·	4,1		970	41		133	41		209	41		-1649	7	-51	41		-1649	1	-120	41		-1649	41		88	41		
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	- 2367	116-	-2367	-617		- 727	-677		2210	-617		2277	-677		139	-611	030	.677		556	-611		1877	-611		-2367	-617		-2367	(19-	307	-677		865	1 9 -	275	-677		-375	-617		-2367	-677		
	-1197	0 5 1 .	323	-130		603	-130		-502	.130		336	-130		515	-130	200	-130		-682	-130		380	.130		899	-130		617	130	-121	-130		-954	061-	- 98	-130		999	-130		-763	-130		
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-215	914	285 -215	-1105	585	-215	-1105	585	-215	914	582	-215	698	585	-190	-1051	585	1961	585	-190	.1051	585	.368	1071	585	-215	-1105	585	-215	-1105	ה ה ה	-215	585	-215	-1105	-215	34	585	-215	486	585	-215	-1105	585	-215	
-2854	-262	3 / 2 - 2854	-124	372	-2854	-1318	372	-2854	-362	372	-2854	-1264	372	-3017	-1264	372	120	372	-3017	-1264	372	-2151	420	372	-2854	-1316	372	-2854	32	215	760	372	-2854	954	3/2 -2854	-1018	372	-2854	547	372	-2854	-1318	372	-2854	
1329	65	. 45 - 1329	190	- 36	-1329	95	-36	1329	.1726	- 36	1329	-837	- 36	-1329	1498	35	6751	.36	1329	1092	- 36	-1329	725	-36	-1329	-616	.36	-1329	.678	97.	-1329 -	-36	-1329	-1726	-36 -1329	-1726	-36	1329	-227	-36	1329	-238	-36	1329	
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255	0	25.5	2	.1945	252	0.01	. 255	}	.1945	-255		-1945	255		200	7	-1945	-255		-1945	.255		1558	. 255		-1945	-255		244	CC7.	-1945	-255	1486	-255		-1894	-255		-1945	-255		-1945	-255		-1945	-255
12	ć	302	:	77	.12	.00	- 12	;	.50	-12		-388	-12	Ç		3	-689	-12		-729	.12		404	-12	•	-1702	.12		20/1-	71-	-1702	-12	352	-12		-83	.12		-175	-12		-1702	-12		548	-12
27	(33)	27	:	-1663	27	1361	27	•	1442	27		26	27		27	;	-1070	27		1558	27		1191	27		1412	27	6	299	Ň	-115	2,7	-427	27		419	27		301	27		571	27		786	27
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-335	000	6302.	:	1152	- 335	.1571	- 335		. 70	-335		538	-335		7)	983	-335		-2025	-335		-	-335		-2025	-335		316	ה ה	1289	-335	1399	-335		719	-335		329	-335		~	-335		-286	-335
73	33.0	0.73	•	-228	.73	ď	; ;	•	.1763	-73		-1763	.73	6	201		- 902	-73		80	.73		-27	.73		199	-73	,	0 ~	1	-1763	.73	-1763	-73		353	-73		099-	-73		20	-73	,	-1763	-73
4.1	1640	41.	:	-1649	41	1649	<u> </u>	!	-1649	41		-1649	41	110	14	;	754	41		-494	41		-1649	41		.615	41	0731	6407-	ř	-1649	41	88	41		.1599	11		-1649	41		-1649	41			41
.164	166	.164		-644	. 164	1854	-164	· •	-5 <u>-</u>	-164		-1854	-164	671	164	,	767	-164		-1854	-164		1168	-164		-31	-164	7001	PC07-		- 98	-164	.11	-164		.91	- 164		1314	-164		849	-164	;	606	-164
-677	7367	.677	ı	1285	.677	200	-677		1112	-677		-2367	-677	720	.677		492	-677		1029	-677		-2367	-617		1122	-677	1361	.677	•	1485	-677	-2367	-677		677	-677		-2367	-677		598	-677	ļ	929	-677
-130	13	.130		-429	-130	119	.130		-1472	-130		478	.130	909	-130		135	-130		-1820	.130		-125	-130		732	-130	0	000	2	-12	-130	-337	-130		108	.130		-1371	-130		251	-130	Š	426	-130
436	. u	. 4 . 6	•	-641	436	-647	438	•	483	438	•	192	438		4	•	-118	438	٠	-1252	438	•	-347	438	•	-1252	438	* 0	4.4		537	438	784	438	•	.33	438	•	543	438	•	-347	438	• ;	116	438
-635	, 75¢	.635	•	942	.635	-2325	-635	•	841	-635	•	-271	-635	3616.	-635	•	.1675	.635	•	-406	-635	•	629	-635	•	539	-635	• 00	-635	•	-2325	-635	306	-635	•	-2275	-635	•	1262	-635	•	-221	-635	• •	-1156	-635
585	.1105	585	.215	.1105	585	.1105	585	-215	-286	585	-215	1011	585	-1105	585	-215	-1105	. 585	-215	1071	585	-215	829	585	-215	-1105	585	-215	283	-215	-1105	585	-1105	585	-215	-1055	585	. 359	-1105	582	-215	-1105	585	.215	-1105	585
372	.2954 1318	372	-2854	-1318	372	327	372	-2854	.1318	372	-2854	-262	372	אנטי.	372	-2854	.714	372	- 2854	. 225	372	.2854	.476	372	-2854	-1318	372	-2854	372	-2854	7	372 . -2854	-288	372	-2854	840	372	- 6183	- 33	372	-2854	537	372	-2854	957.	7.5
. 35	1329	36	-1329	.862	96.	-1726	- 36	-1329	-1726	-36	.1329	.1726	. 36	756	.36	.1329	.1726	-36	1329	.1726	-36	-1329	.1725	- 36	-1329	-516	- 36	9261-	.36	-1329	1696	-36	.258	-36	-1329	-629	- 36	4761-	644	- 36	1329	-1726	- 36	1329	97/1.	e.
352	732	.352	.732	1046	.352	1404	-352	.732	-740	-352	- 732	836	- 352	267.	-352	-732	914.	-352	-732	.1126	. 352	-732	.423	.352	. 732	425	- 352	- 732	. 352	-732	-821	.352	-2042	-352	.732	-1992	-352	26/-	1811-	-352	- 732	- 282	.352	287-	505	755.
178	97501-	. 178	-10579	259	.178	10575	.178	-10579	-797	-178	-10579	978	178	518	.178	-10579	1159	.178	-10579	1345	-178	10579	.195	-178	10579	-548	8/1-	42B	-178	-10579	685	-178	-1868	-178	-4397	-1818	-178	BOCOT	65.	8/1-	10579	-118	-178	6/501	911.	.1/8
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0081.	5.55		1098	-255		184	607.	-1847	-255		-1847	.255		-1847	-255	1	1222	3	-1847	-255		.1847	-255		-1998	-255	;	1166	-255	1392	-255		-213	. 255	1712	-255		391	-255		-1945	-255		-1945	-255		-1945
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1880	135		9261 -	335	ŧ	5 C	555.	692	-335		-1279	-335		-1928	-335		21.67		-115	- 335		-875	-335		63	.335	. ;	/ 8 -	-335	1030	-335		-537	- 335	-2025	-335		-2025	-335		15	-335		1131	-335		-1204
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1560	.130		411	-130	,	9,0	05.4.	-774	-130		66-	-130		438	-130		110		648	-130		1053	-130	٠	1133	-130	;	7 6	130	142	-130		522	-130	116	-130		784	-130		-611	.130		27	-130		228
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969	585	263	.1008	585	-174	200	-174	1400	585	-174	2391	585	-174	404	585	-174	200	-174	168	585	-174	.1008	585	- 322	-1058	585	-193	9811	-193	-1058	585	-193	186	-349	1105	585	-215	-1105	585	-215	-1105	585	-215	-1105	585	-215	-286
1182	372	2587	.1221	372	.3136	017.	3/2	219	372	-3136	4	372	-3136	- 317	372	.3136	372	-3136	.1221	372	-3136	-1221	372	-2321	-1211	372	-2999	1/21-	172	1271	372	.2999	-1271	3/2	-258	372	-2854	-1318	372	-2854	-1318	372	-2854	922.	372	-2854	. 58
1175	35	1329	1442	.35	-1329	49¢1	13.70	757	- 36	-1329	-159	-36	-1329	-161	.36	-1329	7257	-1329	-1629	-36	-1329	-1629	- 36	-1329	138	. 36	-1329	687	- 36	1082	-36	-1329	-1679	- 1329	57	.36	-1329	'n	-36	-1329	1298	-36	.1329	-1726	.36	-1329	-678
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4,	.178	-10392	449	-178	10445	1191	10446	-1771	178	10446	17	-178	-10446	534	.178	10445	.178	10446	78	.178	-10446	-1771	.178	.10446	•610	.178	-10516	9 1	.10516	7.3	-178	-10516	1297	-10516	618	-178	-10579	480	-178	10579	-518	-178	10579	-176	-178	10579	.217
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-124	-124	-124	-54		-124	-54		-124	-54		-124	٠	
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1150	.130		-564	-130		.51	-130		-49	-130		-123	-130		585.	-130	-440	-130		- 705	-130		-826	.130		-607	.130		-333	-130		28	-130	,	619	27	-205	-130		6 0	-130		-240	-130		-225	-130
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и 7.	37.2	3938	333	372	-4217	558	372	-4217	138	372	-3817	-50	372	-4214	27.2	3/5	286.	172	-4213	-285	372	.3832	-129	372	-4189	447	372	-4189	1405	372	-4198	-100	372	-4198	323	-3932	237	372	-4191	-321	372	-4125	-313	372	-4178	. 265	372
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7	352	732	.1005	-352	-732	-482	- 352	- 732	- 984	- 352	-732	.1013	.352	-732	576.	ברני. כנר	1010	- 352	-732	-1010	. 352	-732	-1047	-352	-732	-1047	-352	-732	-578	-352	. 732	-1036	.352	.732	6/4.	-732	.537	.352	-732	.1045	.352	-732	-1038	.352	.732	-678	-352
.345	178	-3947	- 24	.178	-8892	-294	-178	-4839	-737	-178	-5500	- 492	.178	-4068	. 425	2000	113	-178	.8901	-836	-178	-8901	-874	-178	-8983	.451	.178	.5767	.863	.178	· 8960	-863	-178	- 8960	100.	.5897	.877	.178	- 6679	- 93	-178	-5572	-435	-178	.7849	-864	-178
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NOTE		-8455																		
NULE		-1558	82	338	-294	453	-1158	197	249	905	-1085	-142	-21	-313	45	531	201	384	-1998	-644
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	-270	•	-2550			-														
-	-1764	3160	-1674	-1340	1700	-1682	1673	-1725	-295	-1758	-2350	-600	-2309	-637	-1338	480	-794	-2035	-2704	2803
•	506	979	.178	-352	-36	372	585	-635	438	-130	-677		41		-335	-54	27	-12	-255	-97
1	-77	-15613	-4261	-732	-1329	-2287	-331	-270	•											
7	-957	2346	-1301	1115	-22	-323	636	-1168	1212	-252	-1982	-382	-1185	610	-420	208	64	.1221	-2252	-1904
		979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•		-15573	-9567	-732	-1329	-1934	-438	•	•											
m	-2152	4599	-1636	156	-414	-1723	375	- 788	352	-901		-1268	-4147	-151	-1003	-39	-838	-1358	-1118	-625
•		919	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	- 73	-335	- 54	27	-12	-255	-97
•		-15622	-7638	-732	-1329	-5068	\$4-	•	•											
4	-720	2689	-528	626	-2137	188	851	-1097	754	-1482	-1778	571	-1203	217	-357	1008	- 79	-1286	-2273	-1606
,	206	919	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•		-15617	- 7828	-732	-1329	-5215	-39	•	*								•			
'n	-1677	2191	-336	1680	265	328	2152	-1198	735	-654			-4319	384	-175		-1323	-1243	-2307	968-
•		979	-178	-352	- 36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•		-15614	-6520	-732	-1329	-5591	-30	•	•											
•	-1507	4373	-2740	-2041	- 869	- 59	1732	- 942	935	-840		-1428	-3558	419	-389	-82	-1097	-2118	-2409	-1925
•		979	-178	-352	.36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
		-15598	-6415	-732	-1329	-6404	-17	٠	*											
1	-710	103	-725	-770	737	2061	1259	-878	424	-1020			-2666	231	689	-326	-761	-1093	-1783	-1335
•		979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•		-15581	-5811	-732	-1329	-6487	-16	*	*											
6 5	-1181	1024	-3207	-2139	1300	-2173	1740	-178	2484	-947	-1441	- 905	-3204	-982	672	-193	-565	-1120	-2572	-1074
٠		979	-178	-352	-36	372	. 585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•		-15554	-5582	-732	-1329	-5831	-26	*	•											
σ.	836	1020	-1939	-2169	781	-473	2628	-516	-829	-1045	-1594	-1030	-2509	355	256	1021	334	-670	-1662	-1614
•	206	979	-178	-352	-36	372	585	-635	438	-130		-164	41	-73	-335	-54	27	-12	-255	-97
•	-117	-15524	-3683	-732	-1329	-7321	ο,	•	•											

-617	-97		.483	-97		-432	-97		-378	•	
-775	- 255		-641	-255		-590	-255		-537	*	
1818	-12		146	-12	•	-348	-12		-294	•	
-494	27		-160	27		-97	27		1973	*	
942	-54		879	-54		1646	-54		-336	•	
-855	-335		-444	-335		0.49-	-335		-617	•	
- 593	-73		-459	-73			-73		-355	•	
-480	41		-345	41			41		-241	•	
	-164		-36	-164		-500	-164		-446	•	
-1197	-677						-677				
-503	-130		-516	-130		-466	-130		-412	•	
	438					102	438	•	156	•	0
-1155	-635										
65	585	- 66	199	585	. 64	249	585	-61	303	•	٠
	372										
	-36										
.872	-352	- 732	-305	.352	-732	-688	-352	-732	-634	•	٠
-669	-178	-2089	1278	-178	-2998	-514	-178	-3348	-460	•	•
459	919	-6982	593	919	-6474	644	616	-6305	697	•	*
-314	206	-402	-180	206	-212	381	506	-170	- 16	٠	*
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	-1099	-97		-61	-97		7.8	-97		-13	-97		- 951	-97		-951	-97		-951	- 97		-907	-97		-907	-97		-894	-97		1279	.97		-743	- 97		-712	-97		- 706	-97		-682	-97	
	-1257	-255		-1257	-255		867	-255		-314	-255		-1110	-255		-1110	-255		2591	-255		681	-255		404	-255		-1052	-255		2283	-255		-901	-255		-870	-255		-864	-255		3347	-255	
	47	-12		-834	-12		-344	-12		859	-12		-55	-12		-502	-12		-691	-12		1473	-12		- 94	.12		1020	-12		95	-12		1847	-12		-628	-12		79	-12		115	-12	
	623	27		412	27		18	27		368	27		933	27		-528	27	•	1097	27		160	27		1536	27		-195	27		936	27		-129	27		-360	27		-583	27		823	27	
	533	-54		137	-54		-184	-54		-947	-54		-909	- 54		-52	- 54		-480	.54		. 864	ţ.		-273	,54		508	45.		-239	-54		-372	-54		-178	- 54		561	-54		700	- 54	
	-1337	-335		-1337	-335		-1228	-335		-418	-335		-929	-335		-1190	-335		-1190	-338		-1145	-335		-1145	-335		.1132	-335		-838	-335		-199	-335		903	-335		- 944	-335		- 70	-335	•
	1183	-73		-188	-73		619	73		-282	-73		2454	- 73		592	-73		-355	.73		-883	. 73		901	-73		-870	-73		-844	- 73		٦	-73		1998	-73		118	-73		-658	-73	
	- 962	41		-962	41		926	41		35	41		171	41		-814	41		828	41		- 770	41		893	41		292	41		1798	41		24	41		-575	41		-569	41		-544	41	
	-1166	- 164		-1166	-164		-1058	-164		-1058	-164		-1019	-164		-1019	-164		-1019	-164		- 975	-164		746	-164		-961	-164		-935	-164		-810	-164		- 780	-164		-774	-164		-749	-164	
	-1679	-677		494	-677		-1570	-677		-1570	-677		88	-677		-1531	-677		-1531	-677		-1487	-677		-1487	-677		-1473	- 677		-1447	-677		-1323	-677		-1292	-677		-655	-677		-1262	-617	
	-421	-130		1166	-130		-328	-130		265	-130		-636	-130		1400	-130		-617	-130		-657	-130		-488	-130		143	-130		069-	-130		514	-130		-182	-130		1016	-130		-583	-130	
•	1796	438	•	427	438	•	-456	438	•	779	438	•	-417	438	•	755	438	*	-49	438	•	1707	438	*	99	438	٠	-359	438	•	-333	438	*	-208	438	•	-178	438	*	287	438	•	-7	438	•
•	-1637	-635	•	.1637	-635	•	-1529	-635	*	-1529	-635	•	-919	-635	•	-448	-635	•	-311	-635	•	966-	-635	•	-1446	-635	•	-1432	-635	•	-1406	-635	•	-778	-635	•	-431	-635	•	869	-635	*	-392	-635	•
-116	-417	585	-116	-417	585	-116	-308	585	-106	-308	585	-106	-270	585	-102	270	585	-102	-270	585	-102	-225	585	96-	-225	585	96.	-212	585	- 93	-186	582	-91	-61	585	-84	-30	585	- 78	-24	585	-77	0	585	-74
-3696	-630	372	-3696	-630	372	-3696	-521	372	-3825	-521	372	-3825	-483	372	-3876	-483	372	-3876	- 50	372	-3876	-438	372	-3960	-235	372	-3960	-425	372	-3996	-399	372	-4034	-274	372	-4148	-243	372	-4251	-237	372	-4274	-213	372	-4319
-1329	695	-36	-1329	-382	-36	-1329	1741	-36	-1329	-629	.36	-1329	-891	-36	-1329	-891	-36	-1329	-891	-36	-1329	-846	-36	-1329	-846	-36	-1329	-833	-36	-1329	-807	•36	-1329	-682	-36	-1329	159	- 36	-1329	-645	-36	-1329	-621	-36	-1329
- 732																																		-998											
- 9205	-1181	-178	- 9205	-187	-178	-2913	-1072	-178	-8972	-1072	-178	-4185	-1033	-178	-8883	-1033	-178	-8883	-1033	-178	-3915	- 989	-178	-8775	-989	-178	-5378	-363	-178	-4564	-949	-178	-2545	-825	-178	-3997	448	-178	-5973	-788	-178	-4279	- 764	-178	0962-
-8205	-23	979	-8205	2846	979	-8205	1662	979	-7972	3161	979	-7972	1019	979	-7883	2054	979	- 7883	125	979	-7883	2183	979	-7775	1556	979	5777.	3140	979	-7738	1100	979	-7670	333	979	-7341	364	979	-7251	370	979	-7235	394	979	-7154
ŗ	-143	206	۲.	- 196	206	-211	482	206	۷,	-688	206	-88	461	206	٠,	46	206	6-	1236	206	-106	-195	206	-10	-605	206	-42	-101	206	-69	- 265	206	-280	-440	206	-103	-410	206	-33	-403	206	-86	-379	506	-210
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-97	•	-1299	- 97		-1299	- 97		57	-97		176	-97		-1207	-97		1045	-97		-1148	-97		744	-97		253	- 97		1994	-97		212	, f.		-1128	-97		-1099	-97		-1099	-97		-1099	-97
-255	:	. 13	-255		-1457	-255		1193	-255		-1387	-255		1973	-255		1487	-255		1824	-255		1484	-255		540	-255		-1360	-255		-1321	5 57-		-1286	-255		1278	-255		-1257	-255		1184	-255
-12		317	-12		697	-12		392	-12		226	-13		-34	-12		1642	-12		-67	-12		- 205	-12		-315	-12		-297	-12		1,74	71-	,	-259	-12		-834	-12		-185	-12		504	-12
27	!	427	27	٠	2009	27		1001	27		-73	27		615	27		-121	27		1402	27		832	27		1686	27		297	27		-157	1.7		469	27		-339	27		976-	27		-81	27
-54	:	1041	-54		184	-54		-1221	-54		205	-54		1749	-54		16	-54		674	-54		598	-54		267	-54		566	-54		1252	-54		-579	-54		25	-54		-1056	-54		-1056	-54
-335	!	-1537	-335		-196	-335		-1502	-335		-1467	-335		-1445	-335		-1425	-335		-1387	-335		-1504	-335		-1472	-335		-1440	-335		-1401	-332		-1366	-335		-1337	-335		-1337	-335		-1337	-335
-73		-21	-73		-1275	-73		666	-73		1109	-		603	-73		37	- 73		-1124	-73		-398	-73		-519	-73		-1178	-73		64	-73		1591	-73		619	-73		129	-73		-1075	-73
41		567	41		14	41		-168	41		-89	41		-475	41		-586	4		-787	41		438	41		-119	41		1128	41		212	~! *		1460	41		323	41		- 269	41		-405	41
.164		-1367	-164	٠	-1367	-164		-523	-164		-634	-164		-1275	-164		-1255	-164		377	-164		-614	-164		126	-164		-1270	-164		547	-164		-1196	-164		250	-164		-519	-164		1636	-164
176.		893	-677		116	-677		-1844	1-677		-1809	-677		-1787	-677		-1767	-617		192	-677		-1846	-617		-1813	-677		-325	-677		-1743	-677		-1708	-677		827	-677		-1679	-677		1182	-677
.130		-1333	-130		-351	-130		946	-130		191	-130		415	-130		252	-130		-123	-130		-642	-130		173	-130		249	-130		-537	-130		564	-130		1160	-130		1518	-130		-182	-130
438	•	368	438	•	- 765	438	•	15	438	•	1501	438	•	28	438	•	44	438	•	732	438	•	954	438	•	87	438	٠	20	438	•	-158	438	*	1021	438	*	-564	438	•	539	438	*	1186	438
-635	•	-1838	-635	•	-1838	-635	•	-1802	-635	•	-1768	-635	•	-1746	-635	•	-1726	-635	٠.	-1687	-635	•	-1805	-635	*	-1772	-635	*	-1741	-635	•	-1701	-635	4	-1371	-635	•	-1637	-635	•	-1057	-635	*	-1637	-635
585	- 205	-617	582	-205	-617	585	-205	-582	585	-187	-547	585	-241	-525	585	-226	-505	585	-169	-467	585	-399	-584	585	-200	-552	585	-184	-520	585	-170	-481	585	-143	-446	582	-135	-417	585	-116	-417	585	-116	-417	583
27.8	-2913	1090	372	-2913	-830	372	-2913	- 195	372	-3040	- 760	372	-2699	-738	372	-2786	-718	372	-3178	-680	372	-2049	-197	372	-2949	-349	372	-3064	-733	372	-3169	-481	372	-3408	-629	372	-3485	-630	372	-3696	-630	372	-3696	-630	372
- 36																																													
-352																																													
-178	-9617	-1381	-178	-9617	-1381	-178	-4553	-1346	-178	-4558	-1311	-178	-4319	-1289	-178	-4196	-1269	-178	-4370	-1230	-178	-9333	-1348	-178	-4661	-74	-178	-4682	-464	-178	-4267	-858	-178	-4484	-1210	-178	-4528	-385	-178	-9205	-439	-178	-9205	.1181	-178
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-1367	-255		-1401	-255		-1401	-255		-1401	-255		-1401	-255		-1401	-255		-1401	-255		-1401	-255		-1401	-255		-1457	-255		-1457	-255		-1457	-255		-1457	-255		1225	-255		1128	-255		1284
.1125	.12		.1158	-12		-1158	-12		-795	-12		-360	-12		-819	-12		-33	-13		-1158	-12		-1158	-12		-662	-12		116	-12		-27	-12		-272	-12		-1031	-12		-20	-12		549
1034	27		1353	27		276	27		-1119	27		-1119	27		-383	27		-632	27		717	27		-186	27		295	27		-351	27		620	27		379	27		337	27		204	27		342
- 59	- 54		545	-54		-260	-54		602	- 54		505	-54		475	-54		-927	-54		-1200	- 54		-145	-54		326	-54		175	- 54		564	-54		-1257	-54		-535	-54		294	- 54		994
-1447	-335		.1481	-335		- 769	-335		-1142	-335		-1481	-335		-61	-335		-1481	-335		-1481	-335		-847	-335		749	-335		-1537	-335		-641	-335		-1537	-335		-1537	-335		-1537	-335		-1537
-1185	.73		-1219	-73		-375	- 73		1161	-73		40	-73		157	-73		-649	-73		445	.73		185	- 73		-333	-73		512	-73		779	-73		576	-73		1287	-73		983	-73		-436
- 20	41		-1105	41		876	41		995	41		237	41		13	41		-436	41		-1105	41		-1105	41		-77	41		-137	41		792	41		-259	41		108	41		-129	41		-1162
900	-164		-1310	-164		9	-164		558	-164		-1310	-164		1178	-164		57	-164		234	-164		-136	-164		- 925	-164		-1367	-164		-1367	-164		-1367	-164		78	-164		278	-164		-30
780	-677		-1822	-677		-1822	-677		-1822	-677		-1822	-677		263	-677		-1822	-677		-1822	-677		-1822	-677		-213	-677		597	-677		-1879	-677		-1879	-677		-1879	-677		-1879	-677		-1879
-1243	-130		476	-130		116	-130		-374	-130		768	-130		312	-130		265	-130	•	279	-130		212	-130		374	-130		690	-130		-263	-130		359	-130		1113	-130		498	-130		-139
1383	438	•	106	438	•	-35	438	•	141	438	•	447	. 438	*	-429	438	*	829	438	•	794	438	•	695	438	•	-47	438	*	67	438	•	-34	438	•	-122	438	*	711	438	*	613	438	•	1275
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1587.	-164		1162	-164		928	-164		-578	-164		384	-164		236	-164		-2277	-164		-2277	-164		-2248	-164		-2035	-164		-2149	-164		-292	-164		-2005	-164		-1921	-164		-1837	-164		-1759
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962	-178	-4750	1278	-178	-11258	226	-178	-5580	1303	-178	-5291	-28	-178	.11192	746	-178	-6494	-63	-178	111176	-111	-178	111176	433	-178	11176	630	-178	-3112	-817	-178	-4768	- 786	-178	-3504	764	-178	-3747	115	-178	-3724	-1851	.178	-3800	-558
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- 2550 -	7 7 7	١.	-2550	-255		- 5250 -	-255		-2550	-255		S.	- 255		-2550	-255		217	-255		0	-255		-2550	-255		-2516	-255		-2516	-255		-2516		•	-255		1328	-255		741	-255	
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-4123	יייייייייייייייייייייייייייייייייייייי	4123	-745	372	-4123	-1923	372	-4123	-892	372	-4123	-1923	372	-4123	-1327	372	-4123	- 793	372	-4123	-108	372	-4123	-1028	372	-4123	- 76	372	-4197	-1889	372	-4197	- 1889	4197	- 893	372	-4197	-320	372	-4197	-1851	372	-4265
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-732	2 6	- 732	1241	-352	-732	440	-352	-732	358	-352	-732	178	-352	-732	715	-352	-732	-247	-352	- 732	592	-352	-732	603	-352	-732	-123	-352	- 732	-2614	-352	-732	774	255-	580	-352	-732	1210	-352	.732	552	-352	-732
-11401	1 0	-1140}	-205	-178	-11401	553	-178	-11401	1224	-178	-11401	606	-178	-11401	-236	-178	-11401	1220	-178	-11401	433	-178	-11401	1170	-178	-5149	1271	-178	-11360	1657	-178	-11360	363	מאבוני	758	-178	.11360	218	-178	-4966	382	-178	.11313
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-255		-2575	-255		-2582	-255	-	-2582	-255		-2589	-255		-2556	-255	-	-2556	-255		-2556	. 255		-2589	-255		-2589	-255		-2589 -	-255		-2589	-255		-2589	CC7-	-2589	-255))	-2550	-255		1137 -	-255
-12		258	-12		-2340	-12		-77.	-12		- 809	-12		-2275	-12		-933	-12		622	-12		-173	-12		280	.12		220	-12		-994	-12	3	9 ;	71.	-1203	-12	}	-2307	-12		-2307	-12
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.54		341	-54		1191	-54		85	-54		-1486	-54		-65	-54		313	-54		31	- 54		-1032	- 54		-685	-54		-866	- 54		-2085	-54		2501-	P	-844	.54		.1063	-54		13	-54
.335		-695	-335		906	-335		409	-335		260	-335		751	-335		-257	-335		454	-335		-193	-335		35	.335		-1413	-335		-253	-335	•	יי פרי	6	128	-335		340	-335	٠	-735	-335
- 73		1318	. 73		515	- 73		728	-73		1333	-73		912	-73		512	-73		637	- 73		1013	-73		1029	-73		1217	-73		1437	-73	;	416	•	903	-73	,	-329	-73		.1770	-73
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438	•	866	438	•	-148	438	•	1171	438	•	377	438	•	1140	438	*	259	438	•	-617	438	•	286	438	•	270	438	•	1093	438	•	627	438		900	•	691	438	•	984	438	*	707	438
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372	-3795	-471	372	-3814	-494	372	-4065	-221	372	-3822	-1962	372	-4043	-1929	372	-4112	-1287	372	-4112	- 754	372	-3288	-817	372	-4043	-865	372	-4043	-827	372	-4043	- 1961	372		. , , , , ,	2000	-868	372	4008	- 935	372	4123	1923	372
- 36	-1329	63	-36	-1329	-638	-36	-1329	105	-36	-1329	-269							-36		-519	-36	-1329	-396						331				-36	200	626	1330	135	-36	.1329	-509	-36	.1329	96	-36
-352																																	-352				-811					-732	452	-352
-178	-11420	708	-178	11431	33	-178	11439	-2506	-178	11439	-398	-178	-5207	-493	-178	11408	-647	-178	11408	1190	-178	-11408	444	-178	11448	558	-178	11448	-516	-178	11448	1501	-178	05577	97.0	8670L	1498	-178	-4957	194	-178	11401	672	-178
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-2658	-335		-654	-338	•	1193	-335	,	334	-335	9	806	-335		15.	-335		894	-335		606	-335		1334	-335	,	1269	-335	,	1661	-335	Ş	4 G	-335	7.00	, ,	٠3.5.	,	868	-335		841	-335		1309
410	-73		-174	-73		599	-73		946	- 73	ì	- 96	-73		-519	-73	;	341	-73		258	-73		1538	-73		657	-73		978	-73		1230	-73	00.	77.	-73		633	-73		-710	-73		1187
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ά		*	536	438	•	802	438	•	1559	438	•	1015	438	*	961	438	*	1049	438	•	730	438	•	177	438	•	882	438	•	1559	438	٠,	470	438	+ 8	120/	438	*	872	438	•	809	438	•	380
1168	-635	*	883	-635	•	448	-635	•	195	-635	*	-252	-635	•	-720	-635	•	-701	-635	*	-1226	-635	•	-340	-635	•	-422	-635	*	-64	-635	•	495	-635	* I	415	-635	•	- 992	-635	•	-2842	-635	*	-1617
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1001	7561	.4085	.1951	372	-4085	-1951	372	-3258	-1963	372	-4061	-417	372	-2814	6 0	372	-4046	-811	372	-3303	.166	372	-4009	-1977	372	-4041	-126	372	-4067	-694	372	-3262	-1508	372	-4005	-390	372	-4111	-345	372	-4111	431	372	-4129	-471
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ć	170	7271	* C	-178	11434	- 782	-178	-5894	-2514	-178	-5434	- 730	-178	-5310	581	-178	-6814	646	-178	-11440	-1294	-178	-7111	-148	-178	-7300	-1544	-178	-11457	- 969	-178	-10748	-	-178	-4540	-2497	-178	-11429	- 990	-178	-7362	159	-178	-11420	698
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-130	1	1358	061-	383	-130		594	-130		-285	-130		995	-130		843	-130		456	-130		307	-130		-125	-130		489	-130		621	-130		-57	-130		324	-130		-666	-130		15	-130
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585	-121	1004	-121	194	585	-121	649	585	.383	1674	585	-105	-254	585	-270	181	585	-111	438	585	-111	1034	585	-195	1405	585	-118	868	585	-105	380	585	-105	-1798	585	-105	.1838	585	-443	885	585	-131	721	585
372	-3641	2129	-3641	1566	372	-3641	-1332	372	-2102	1036	372	-3836	4	372	-2549	-125	372	-3752	009	372	-3752	-58	372	-2984	1584	372	-3669	-504	372	-3836	.1279	372	-3836	1255	372	-3836	2051	372	.1919	-537	372	.3521	-981	372
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171	.73	2	-694	-73		-488	-73		691	-73		1186	- 73		-1099	-73		192	- 73		1487	-73		-2620	-73		-273	-73		936	-73		457	-73	;	y e. i	٤/-	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	55.7	?	7 70	; ;	1	-137	
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-1084	585	-166	-2007	585	-149	1018	585	-149	2072	585	-444	2721	585	-388	801	585	-293	-1757	582	-150	- 785	585	-144	-1962	585	-349	-1934	583	-214	-1927	585	-361	-277	181	1.57	א מ ט	148	1900	585	-115	136	7.85	-171	820	
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0871.	-335		.358	-335	•	- 808	- 335		- 725	-335		-918	-335		79	-335		-14	-335		-1733	-335		-13	-338		-1010	-335		-857	-335	,	500	0 8 9 1	-644	-335		-961	-335		-2956	-335		
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1397	-623		144	-611		1013	-677		-140	-617		123	-677		-986	-677		-83	-677		-115	-677		-300	-611		-3197	-617		-3197	-677	;	2 4 5	. 0	.1707	-677		-3317	-677		3298	-677		
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254	585	-315	774	585	-196	1368	585	-359	1066	585	-181	400	585	-456	-57	585	-311	-604	585	-273	1562	585	-532	1292	585				-124	-286	585	-124	758	282	1,164	285	-703	-24	585	-229	472	585	-162	
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l Plan9	661	-1000	,	8 B 80 81 81	E<-1		-2269	-352	-2343	-352	-732	-2551	-352	-732	.2584	-352	-732	-1057	-352	-732	-944	- 352	-732	0/87,	300°	-2578	-352	-732	-2629	-352	-732	
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193 Amino no no [converted from an old Plan9 HMM]	0 Mon Mar	-8455	4	ა გ	E^ -	-2869	-1711	506	-1680	206	-39	- 993	206	-27	-2026			-627	206	99-	-1984			900,	907	506-	206	-2	417	206	-39	
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-256		379	-255		717	-255		2176	-255		-1674	-255		95	-271		-1821	-255		-2984	-259		-3617	•	
-29		-1867	-12		-1944	-12		-1159	-12		-1309	-12		-1248	-22		-3386	-12		-1574	-17		-3374	•	
16		-534	27		-745	27		381	27		1290	72		-233	37		77	27		-561	33		-786	•	
-62		-412	- 54		-920	-54		-150	-54		-121	-54		-658	-49		-679	-54		-532	-39		-2177	*	
.319		-1233	-335		-1223	-335		-963	-335		-1154	-335		-510	-320		424	-335		659	-324		-3697	•	
-71		-742	-73		-20	- 73		-978	-73		-577	-73		-1634	-68		-427	-73		-1215	-73		-3435	•	
96		1581	41		1025	41		707	41		- 903	41		-1003	51		-1542	41		-661	34		-598	•	
-173		-615	-164		-214	-164		- 945	-164		-124	-164		-546	-167		699	-164		359	-160		-3526	•	
-684		-2952	-677		-2005	-677		-1562	-677		-1340	-677		-3189	-685		-2693	-617		-3464	-682		-4038	•	
-141		-1481	-130		-2195	-130		-2870	-130		-2646	-130	,	-1749	-138		-1011	-130		-1366	-134		-3492	•	
435	•	-1616	438	*	-1124	438	*	-1794	438	•	-1452	438	*	-143	437	•	-1664	438	*	-1113	432	•	-2924	*	0
-649	•	-3062	-635	*	-2738	-635	*	-1868	-635	*	-2316	-635	•	-2748	-641	•	-2365	-635	•	-3041	-641	•	-3997	•	•
576	ű	-408	585	4.	-323	585	?	-67	585	-10	225	585	ć,	-715	577	2,	780	585	7	183	583	?	-2777	•	*
368	-8971	1091	372	-8563	2378	372	-9247	1135	372	-7202	2152	372	-9055	2353	371	-9492	1515	372	-9355	-2942	366	-9794	-2990	•	*
-45	-10533	-358	-36	-1329	374	-36	-1329	1747	-36	-1329	-149	-36	-1329	1020	-43	-9612	-921	-36	-1329	-1678	-40	-7395	-3398	٠	•
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-171	-4732	-235	-178	-4090	-652	-178	-3954	-354	-178	-3870	-81	-178	-3885	-1092	-170	-2999	515	-178	-2115	251	-181	-1182	-3540	•	•
1052	-58	3598	979	-14801	1229	616	-14698	945	616	-14586	1293	919	-14488	2332	1001	-197	3752	979	-13798	4754	1010	- 852	5631	•	•
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	-2198	-255		-1721	-255		-713	-255		-1637	-281		-3241	-255		-1847	-255		-1992	-255		-1897	-255		-518	-255		-129	-255		96	-255		-373	-255		-1305	-255		-2	-257		-353
	-1057	-12		-1705	-12		- 956	-12		596-	-29		-882	-12		-733	-12		-641	-12		-263	-12		-381	-12		-298	-13		-718	-12		-879	-12		-972	-12		-1454	-10		-2680
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	467	-54		69	- 54		-303	-54		-298	-49		-542	- 54		-653	-54		- 734	-54		-486	-54		-380	-54		131	-54		662	-54		-370	-54		438	-54		-683	-62		-1310
	203	:335		-26	-335		-524	-335		- 949	-332		-548	-335		93	-335		- 539	-335		-31	-335		-759	-335		-661	-335		-1218	-335		-1097	-335		351	-335		-753	-320		-1402
	-336	-73		-84	-73		-23	-73		-334	-59		-297	-73		299	- 73		-872	. 73		- 92	-73		-494	-73		-741	- 73		-487	-73		-809	-73		836	-73		-581	-47		-1185
	829	41		810	41		1753	41		-326	25		-847	41		-1288	41		-554	41		-198	41		443	41		-141	41		35	41		-653	41		~913	41		-364	38		472
	423	-164		1021	-164		613	-164		748	-127		1775	-164		595	-164		1279	-164		-121	-164		412	-164		619	-164		149	-164		-12	-164		- 909	-164		-1607	-175		-1191
	-2433	-677		-1627	LL9		-1708	-677		-1943	-688		-2729	677		-3041	-617		-2061	-677		-3184	-617		-2256	-677		-2017	-677		-1935	-677		-1414	-677		-1406	-677		-1811	-690		-2708
	-1749	-130		-1405	-130		-1241	-130		-2003	-148		-1954	-130		-1195	-130		-2435	-130		-1717	-130		-1773	-130		-1802	-130		-2238	-130		-2679	-130		-2145	-130		-2446	-143		-1542
*	-1580	438	•	-1080	438	•	-1508	438	•	-1620	415	•	-1677	438	•	-1367	438	*	-1699	438	•	-1257	438	*	-1593	438	*	-1496	438	•	-1225	438	*	-1495	438	*	-410	438	*	-1964	423	*	-1704
•	-1688	-635	•	-1493	-635	•	-1881	-635	*	-2075	-663	•	-1750	-635	*	-1396	-635	•	-1557	-635	•	-915	-635	•	-1173	-635	*	-975	-635	•	-1628	-635	•	-2374	-635	•	-1595	-635	•	-2025	-635	•	-3007
-220	126	585	-115	936	585	-51	-254	585	-101	134	597	φ,	277	585	-29	903	585	-15	-150	585	-11	- 760	585	-32	-819	585	-36	340	585	-41	-916	585	-20	-15	585	-15	-162	585	-11	-388	579	Ş	-1228
-2821	872	372	-3708	563	372	-4855	890	372	-3888	453	386	-7564	1151	372	-5676	1709	372	-6622	1837	372	- 7009	1193	372	-5491	1050	372	-5357	944	372	-5163	1141	372	-6192	1366	372	-6625	919	372	-7041	589	360	-8268	374
-1329	- 941	-36	-1329	-1047	-36	-1329	-712	-36	-1329	-499	44-	-11114	969-	-36	-1329	-868	-36	-1329	-1587	-36	-1329	-763	-36	-1329	-825	-36	-1329	-779	-36	-1329	-375	-36	-1329	1416	-36	-1329	179	-36	-1329	636	-50	10708	-1200
-732	-1111	-352	-732	-401	-352	-732	-550	-352	-732	-1000	-358	7	-1015	-352	-732	-485	-352	-732	-411	-352	-732	-748	-352	-732	-1066	-352	-732	-39	-352	-732	-169	-352	-732	-383	-352	-732	-308	-352	-732	-1618	-331	7	- 703
-4279	-534	-178	-4603	4	-178	-4481	- 587	-178	-4637	-134	-176	-4407	-387	-178	-4982	-178	-178	-5192	196	-178	-4937	-342	.178	-4621	58	-178	-5266	121	-178	-5424	593	-178	-5602	-612	-178	-4985	-757	-178	-5899	-1497	-189	-5165	-353
-15724	3544	919	-15669	3343	616	15622	3262	919	15562	4375	1094	- 75	3878	979	15401	3077	979	15362	3112	919	15325	3442	919	15276	3884	979	15226	2771	979	15204	3016	616	15187	2625	979	15165	3236	979	15120	4495	1106	-47	4855
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.213	612	T O	.262	9	3	2775		Š	-447	7	5	- 243	7 4	7	-715	5.5	;	-111	. 5.4	;	242	- 54	;	-772		5	-136	. 5.	;	-442	-54		- 708	- 54		-294	.54	,	-297	. 5.4	;	106	-54	,
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-1407	-130	•	-1849	-154		-1509	-130		-858	-130		-1081	-130		-1861	-130		-1597	-130		-1969	-130		-1290	-130		-1713	-130		-1172	-130		-1680	`-130		-1421	-130		-1554	-130		-1253	-130	
-907	438	*	-2649	405	•	-1442	438	•	-653	438	*	-1236	438	•	-2097	438	*	-1581	438	•	-1123	438	•	-1468	438	•	-746	438	•	-1976	438	•	-1898	438	•	-1695	438	•	-1242	438	•	1118	438	
-1644	-635	*	- 703	-635	•	-1220	-635	*	-1946	-635	•	-1416	-635	•	-1811	-635	*	-1885	-635	•	-1360	-635	•	-950	-635	•	-1495	-635	•	338	-635	•	-1731	-635		-622	-635	•	-2040	-635	•	-1770	-635	
-654	585	-938	-787	999	-898	-112	585	-227	-189	585	-161	-255	585	-243	-430	585	-124	-128	585	-148	-466	585	-203	110	585	-194	-227	585	-479	424	585	-295	-284	585	-176	160	585	-205	-284	585	-111	-150	585	
1371	372	-1065	637	384	-1109	224	372	-2777	247	372	-3241	670	372	-2691	2028	372	-3600	518	.372	-3356	1305	372	-2928	1704	372	-2994	200	372	-1824	611	372	-2437	623	372	-3119	738	372	-2914	470	372	.3750	848	372	
-835	-36	-1329	-821	-41	-11382	-1003	-36	-1329	-460	-36	-1329	-594	-36	-1329	147	-36	-1329	1400	-36	-1329	-142	-36	-1329	385	-36	-1329	-336	-36	-1329	-373	-36	-1329	-623	-36	-1329	-1236	-36	-1329	-528	-36	1329	-1377	-36	
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-31	-178	-3749	-430	-177	-9344	-117	-178	-8989	561	-178	-6793	-18	-178	-7190	-467	-178	-6918	-249	-178	-6995	-626	-178	-5929	- 85	-178	-6041	1200	-178	-6608	653	-178	-6358	1466	-178	-5975	513	-178	-6035	414	-178	-5451	-101	-178	
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	- 206	5 979	-178	-352	-36	372	285	-635	438	-130	-677	-164	41	-73	-338	-54	27	-12	-255	-97
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	2 -1097	1 4294	273	-591	-1829	190	-179	-883	-1847	-1201	-2130	948	-397	184	-1066	-631	-1083	-615	-1242	-1474
	- 179	1601 6	-143	-347	-57	372	595	-649	412	-146	-690	-126	62	-41	-333	-46	80	-37	-289	-109
	7046		-6071	-1	-11285	-2558	-268	•	•											
-	3 -1144	(**)	96	.180	-1019	515	1204	-1205	-1645	-1856	-2683	1848	-622	-122	-240	-394	- 507	-1185	-1847	-943
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-	4 -1063	•	60	. 549	-2315	1691	717	-1290	-1426	-1312	-1821	786	463	371	54	-346	-333	-1609	-3656	-913
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	5 -469	3330	-240	-170	-1205	1710	261	-1770	-1747	-2058	-3115	949	19	-446	-1204	-369	-137	-1083	-1903	-1211
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_	6111- 9	(*)	-349	-267	-1044	926	380	-898	-817	-1515	-1938	9	104	-71	259	-299	830	-260	-3057	-977
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-	7 -964	4380	-351	-862	-856	499	-143	-1459	-1531	-1602	-2239	347	19	-258	-649	-851	-426	-772	-2438	-885
-	171 -	1104	-158	-342	-57	371	579	-611	409	-150	-695	-145	39	-63	-337	-57	4 9	4	-285	-120
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,	- 176	1058	-167	-354	-61	381	570	-640	413	-147	-688	-146	37	-43	-328	- 55	11	-13	-276	-109
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554	1.51		.227	. 164		.227	-164		-227	•	
1055	577		739	-677		.739	.617		-739	•	
520	. 130		305	-130		.193	.130		.193	•	
48	438	•	375	438	•	633	438	•	375	•	0
.392	635	•	.377	.635	•	-698	-635	•	869-	•	•
196	585	.125	525	585	-107	525	585	- 107	522	•	•
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232	3.15		1674	-335		755	-335		-1153	-335		-1153	-335	-1153	.335		-1114	-338		-507	-335		-1140	-335		435	-335		496	-335		.367	- 335	-74	-335		451	-335		1140	-335		1140	-335		.1140	-335
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	-391	- 335		-391	-335		-366	-335		-366	*	
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	- 220	-164		-220	-164		-196	-164		-196		
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	-186	-130		-186	-130		-162	-130		-162	*	
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-642	529	585	-642	529	585	-642	554	585	-583	554	•	•
-1478	316	372	-1478	316	372	-1478	341	372	-1589	341	•	•
-1329	- 92	-36	-1329	-92	-36	-1329	-67	-36	-1329	-67	٠	•
-732	-408	-352	-732	41	-352	-732	-383	-352	-732	147	•	•
-6924	308	-178	-6924	308	-178	-3451	-210	-178	-6810	-210	٠	•
-5924	923	919	-5924	923	919	-5924	948	979	-5810	948	•	•
-36	150	206	-36	150	206	-165	175	206	-39	175	•	•
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113	1		616.	41		-689	41		-689	41		-663	41		-578	41		-513	41		-391	41		-242	41		-242	•:	
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	• -	7 95	-682	-1840	1868	-1691	-1289	1372	-2297	1672	290	214	-1826	-1621	-343	-257	-1029	-1635	-338	-1916	-1758
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	•	٠.	-9591	-10591	-732	-1329	-33	-5451	•	•											
	~	8 1295		-1923	-159	-1780	-1372	-1159	-2379	1375	363	525	-1908	-1704	1301	606	35	-1717	-715	-1999	-1841
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	•	٠.	-9703	-10703	-732	-1329	-76	-4293	*	•											
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	-1370	-255		-1308	-255		-1251	-255		-1251	-255		-1163	-255		-1163	-255		-1163	- 255		-1055	-255		-918	-255		970	-255		-569	•	
	1457	-12		670	-12		388	-12		-418	-12		-921	-12		-921	-12		-680	-12		-768	-12		56	-12		240	-12		-325	•	
	-1088	27		. 72	27		-970	27		-204	27		-882	27		-882	27		-132	27		-329	27		472	27		-149	27		-286	•	
	-1169	. 54		-279	-54		-1050	-54		-677	-54		-241	-54		-965	-54		-713	-54		155	-54		-717	-54		-541	-54		-367	•	
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	336	41		677	41		-956	41		218	41		1258	41		1809	41		1660	41		1226	41		2057	41		-446	41		-272	•	
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**	-530	585	-34	133	585	-33	-411	585	-32	-411	585	-32	Š	585	-32	908	585	-32	464	585	-32	-215	585	-30	- 78	585	- 28	86	585	- 56	272	•	٠
- 5445	-440	372	-5443	-406	372	-5476	-624	372	-5497	-624	372	-5497	-536	372	-5530	-536	372	-5530	275	372	-5530	-401	372	-5608	-291	372	-5702	-115	372	-5819	65	•	•
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- 9/19	1261	-178	-3824	1252	-178	-3914	2902	-178	- 9506	1314	-178	-3271	849	-178	-9338	1534	-178	-9338	1087	-178	-2878	- 935	-178	-2422	-841	-178	-1957	-665	-178	-1749	-492	•	•
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٠	- 506	206	-109	38	206	-103	- 790	506	9-	175	206	-162	-379	206	۲.	-33	206	-7	-331	206	-216	407	206	-304	-457	206	-438	-281	206	-525	-107	•	•
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- 54	ć	, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	,	-1843	-54		818	-54		-896	-54		-971	-54		-371	-54		-576	-54		.730	-54		.750	-54		-383	-54		-124	-54		-1327	- 54		-1851	54		-495	- 54	
-335		-335))	903	-335		853	-335		1005	-335		-485	-335		7	-335		-83	-335		-1037	-335		-2065	-335		98	-335		- 963 ·	- 335		588	-335		-16	-335		-711	-335	
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-130	C	-130) 	650	-130		-1814	-130		-137	-130		-662	-130		-647	-130		154	-130		-382	-130		366	-130		-1178	-130		117	-130		174	-130		265	-130		-540	-130	
4 38 •	ָ ֖֓֞	438	•	-942	438	•	-1295	438	•	-250	438	•	-1125	438	•	208	438	•	-1190	438	•	- 900	438	•	-1342	438	•	-250	438	•	-451	438	•	-1085	438	•	-34	438	•	-361	438	•
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372	0000	372	-3668	334	372	-4247	.500	372	-3478	-627	372	-2989	77	372	-3369	397	372	-3690	344	372	-3620	-1282	372	-3640	-507	372	-4033	-1381	372	-3835	-397	372	-3672	-831	372	-3920	-1425	372	-4103	-389	372	-4103
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206	D 0	206	-13	183	206	.78	-75	206	-194	681	206	177	210	206	-80	-219	206	-61	-545	206	-45	-553	206	-11	-249	206	-19	96-	206	-20	.530	506	-16	-733	206	ņ	-289	206	۳,	- 55	206	-92
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;	641	.97		-1828	-97		899	-97		671	- 97		-1877	-97		-1827	-97		106	-97		1069	-97		-1041	-97		-14	-97		1130	-97		1268	-97		-1878	-97		-1158	-97		671
•	Σħ.	-255		999	-255		-1930	-255		-2035	-255		-2035	-255		-1985	-255		-1934	- 255		-2009	-255		- 2009	-255		-1480	-255		-1830	-255		872	-255		-2037	-255		-2040	-255		-2017
	-52	-12		-516	-12		-940	-12		-271	-12		78	-12		118	-12		40	-12		-478	-12		-413	-12		321			586	-12		707	-12		476	-12		-532	-13		-261
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į	.571	-54		-458			-384	-54		-82	-54		-633	-54		477	-54		336	-54		-701	-54		83	-54		210	-54		-133	-54		-82	-54		-1126	-54		-377	-54		-250
	280	-335		-684	-335		336	-335		528	-335		598	-335		-1425	-335		-568	-335		12	-335		164	-335		491	-335		-258	-335		333	-335		-471	-335		-668	-335		230
;	339	. 73		-121	-73		-111	-73		-901	-73		-1853	-73		-68	-73		-25	-73		1310	-73		-1541	- 73		279	-73		-342	-73		-838	-73		-740	-73		414	-73		504
,	252	41		-751	41		-219	41		-51	41		-910	41		403	41		-1638	41		-1714	41		-1714	41		-127	41		-1714	41		-205	41		693	41		631	41		699
;	33	-164		-518	-164		-143	-164		202	-164		651	-164		-190	-164		-315	-164		-1206	-164		523	-164		-1097	-164		141	-164		534	-164		-384	-164		953	-164		517
,	-647	-677		-1739	-677		-870	-677		-640	-677		-2456	-677		629	-677		-2355	-677		-1957	-677		336	-677		353	-677		-37	-677		-250	-677		-2458	-677		219	-677		-425
;	-485	-130		411	-130		397	-130		-1104	-130		-540	-130		-414	-130	-	-462	-130		342	-130		324	-130		362	-130		-216	-130		-315	-130		577	-130		588	-130		705
•	.5.	438	•	-1294	438	•	-67	438	*	-1207	438	•	651	438	*	-97	438	*	-1040	438	*	-205	438	•	-772	438	•	481	438	•	-82	438	*	548	438	•	-314	438	*	7	438	*	-498
•	-630	-635	*	1162	-635	•	480	-635	•	1436	-635	•	302	-635	•	-2365	-635	*	1053	-635	•	671	-635	•	258	-635	•	38	-635	•	370	-635	*	38	-635	•	332	-635	•		-635	•	558
.134	-615	585	66-	1618	585	-95	-492	585	-157	143	585	-68	-1147	585	-68	-1145	585	-120	-1094	582	-176	677	585	- 70	-1170	585	-70	-345	585	- 70	-1170	585	-107	-439	585	. 78	403	585	-101	-1200	585	-100	-2
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۴.	-862	206	-50	-1526	206	-129	- 794	206	ŗ	-731	206	۴,	-777	206	-69	636	206	-145	578	206	-42	-1286	206	<u>.</u> ب	437	206	ņ	-1082	206	۴.	96-	506	ŗ.	208	206	ű	369	506	-18	391	206	-49	-307
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19	-97	;	-1291	.97		-357	-97		- 798	-97		879.	-97		89	96~		106	-97		493	.97		-1674	-97		-785	- 97		-1715	-97		-878	-97		-1665	-97		-953	-97		-1751	-97
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499	40		180	41		1857	41		-717	41		302	41		320	41		-536	41		-1520	41		-133	41		-720	41		297	41		419	41		437	41		900	41		-1371	41
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282	438	•	-589	438	•	7	438	٠	-326	438	•	-486	438	•	166-	437	•	419	438	*	-869	438	•	257	438	•	-181	438	•	726	438	*.	-189	438	*	770	438	•	29	438	•	572	438
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		-45																																									
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	4 -510		736	-1764	369	-300	-827	1707	-783	-493	-2088	069-	1083	-581	175	-1466	-126	5.5	-1667.	488
	- 206	919	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	- 54	27	-12	-255	-97
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	5 -1108		•	-1726	-75	-175	- 789	216	1610	-834	-2051	1159	-1333	-678	-879	850	874	-493	-1629	197
	- 206			-352	-36	372	585	-635	438	-130	-677	-164	41	.73	-335	-54	27	-12	-255	-97
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	9 -20	•	726	-528	41	643	- 937	-2157	-1084	-1211	794	2032	-167	-34	-440	-1098	604	-277	-1116	-1142
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. 34	.530	585	-34	133	585	-33	-411	585	-32	-411	585	-32	ş.	585	-32	908	585	-32	464	585	-32	-215	585	.30	- 78	585	-28	98	585	-26	272	•	•
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'n	-506	206	-109	38	206	-103	- 790	206	9-	175	206	-162	-379	206	۲٠	-33	206	.7	-331	206	-216	407	206	-304	-457	206	-438	-281	206	-525	-107	•	•
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-1827	-97		-1530	- 97		-1758	-97		-1695	-97		-897	- 97		458	- 97		-1607	-97		-302	- 97		-841	-97		-652	-97		-1110	- 97		-1327	-97		-444	-97		-1259	-97		-1212	-97
-1985	-255		-1939	-255		-1916	-255		-1854	-255		-1817	-255		-1787	-255		-1765	-255		-1.338	-255		-1646	-255		-1613	-255		-456	-255		-1485	-255		-1417	-255		-1417	-255		-1370	-255
876	-12		404	-12		80	-12		640	-12		121	-12		-192	-12		426	-12		177	-12		185	-12		1284	-12		-89	-12		1745	-12		727	-12		1162	-12		999	-12
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-97		-1862	- 97		518	-97		-1830	-97		505	- 61		-1839	-97		-1842	-97		118	-97		208	-97		975	-97		-187	-97	•	828	-97		-1883	-97		- 89	-97		-1894	-97	
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41		236	41		-1206	41		-511	41		-38	41		177-	41		-5	41		-1466	41		393	41		343	41		-1198	41		-430	41		265	41		369	41		219	41	
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	491	.12	,	-1354	.13	-224	-12		-604	-12		-77	-12		-34	-12		605	-15		1315	-12		1006	.12		.36	-12		.2418	-12		-2218	-12		699	-12		באני.	-15		-1222	-12		1382	•	
	-242	27		-1218	27	-1173	27		-702	27		-1017	27		-1077	27		955	27		-419	27		558	27		-231	7.2		-590	27		-2180	27	,	0.61-	2.1	6	0 1	97		-598	27		-1056	•	
	. 744	.54	•	-2451	, 4	-2937	-54		-480	.54		-338	·54		-444	-S4		-1220	-54		476	-54		-1158	-54		- 193	.54		1931	-54		2050	-54		7 7	, 54	ć		ı,		-1264	-54		.1137	•	
	262	.335	;	199	-335	182	.335		683	-335		527	-335		2164	-335		2622	-335		920	-335		1396	-335		-468	-335		.338	-335		-2541	-335		7/77-	- 335	,	7707	- 335		1811	-335		-1418	•	
	2265	.73	:	3029	67.	730	-73		-2890	-73		-2086	-73		-505	-73		336	.73		2397	-73		-2768	-73		-1887	-73		-2479	-73		107	.73	;	; ;	- 73	900		٢/٠		438	-73		-1156	•	
	345	4		1819	41	2349	41		9	41		-915	41		-915	41		-2701	41		-2659	41		-743	41		-547	41		-2365	41		699	41	9) pr	4	1330	9,71	1		-1169	41		-401	•	
	-207	- 164	į	409	164	-856	-164		366	-164		1239	-164		2425	-164		-2159	-164		-2131	-164		128	-164		-652	-164		-1096	-164		-742	-164		BC 7	-154	(631		-164		1391	-164	;	-480	•	
	.138	.617	;	3590	10	-3560	.677		-3494	.677		-1940	-677		-3494	-677		-3418	-677		18	-611		-3372	-677		226	-677		411	-677		-2883	-677		CT07-	//9-	2616	0 1 7	//9-		-1886	-677	;	-1760	•	
	(-	-130		.1109	061.	1260	-130		1601	-130		-366	-130		-1696	-130		-2470	.130		-1873	.130		-1867	.130		-2302	-130		-2536	-130		-2336	-130	•	/907-	051-	0031		151-		-1340	-130	:	-1213	•	
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.2738	1254	372	.3399	- 1442	1199	.540	372	-3463	-2045	372	-3582	910	372	-3582	-893	372	-3582	-278	372	- 3692	-2328	372	.3161	-2323	372	.3788	-2174	372	-3678	-1688	372	9098	-1271	372	2854-	6001.	2/2	1087		7/5	-5660	-838	372	-5736	-711		•
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732	3256	352	732	3256	266.	.2561	-352	. 732	-567	- 352	. 732	-3169	-352	-732	-423	.352	-732	.1181	. 352	-732	.1253	-352	-732	.200	-352	-732	-443	-352	-732	- 738	.352	-732	-465	-352	107		265-	191.		000	- 60	-892	-352	-732	714	•	•
4719	3092	.178	-12113	1195	-5654	.1276	-178	.4602	-2995	-178	-11995	.51	-178	11995	.980	-178	-4469	.1181	.178	-5310	.880	-178	-4997	-2874	-178	.3443	-2724	.178	-3420	-2584	.178	-3186	-2385	-178	6602	22	0.17.	6171		6/1.	5617.	-219	-17B	-2943	B+L		•
-111147	.1935	979	-11113	- 1935	۶/۶ ·	-1904	979	-11076	-1838	919	-10995	-1838	979	-10995	480	979	-10995	-1762	97.9	-10900	.1721	979	-10846	.1716	616	.10841	.1566	616	-10647	1427	979	10455	.1227	979	65101.	0.00	6100	480	0 0		7/5.	-231	979	-8842	-104		٠
.57	1402	206		.2708	907	-688	206	-61	32	206	7	-127	206	7	-477	206	-67	52	508		230	206	-47	-15	206	.140	1553	206	.142	1656	206	. 169	-260	206	900	900	977	910	200	0 7	- 36 /	-1004	206	-205	1.18.		•
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-255		. 3146	-255		-3147	-255		295	-255		-3143	.255	,	538	- 555	,	, , , ,	967.	-2581	-255		657	-255		359	-255		-3272	-255		33	-255		-3327	557-	1226	-255		2834	-255		3768	-255		356	-255		-3197	-255
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7.2		-212	27		.1204	27		-2853	27		-817	27	,	-2148	1.2	Ş	D 1	0,7	258	27		.376	27		-2299	27		-602	27		-197	27	,	-647		-819	27		-614	27		-1044	27		-1504	27		-61	27
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.130		-1727	-130		-1517	.130	:	- 2569	-130		-1765	-130		-1038	-130		1977-	-131	-172	-130		- 84	-130		119	-130		1251	-130		-463	-130	:	-1103	-130	-1291	-130		-1958	-130		-387	.130		-1228	-130	,	-646	-130
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585	-270	1171	585	-379	-822	585	-313	.2295	585	-381	821	582	-120	-1250	585	557-	1502	נטני.	231	585	-290	1933	582	-1173	51	285	-402	-263	585	-435	-	585	-337	1658	285 -192	579	585	-326	265	585	-215	54	582	-200	65	585	-188	108	585
372	.2551	1714	372	-2114	926	372	2358	1888	372	.2107	-1215	372	.3646	-2442	372	- 3312	9 1	215	1954	372	-2458	.1663	372	- 846	45	372	-2040	-677	372	-1941	. 2224	372	-2262	964.	3004	-2700	372	-2306	.2710	372	-2855	-2242	372	-2947	-1422	372	-3034	.628	372
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.352	. 732	1557	-352	-732	2040	-352	-732	1349	-352	- 732	1918	-382	-732	1325	-352	757	2250	255	999-	-352	.732	751	-352	-732	1795	-352	-732	. 92	-352	- 732	-3396	.352	-732	6//-	.732	-3424	-352	-732	-3434	-352	. 732	-3412	.352	-732	-3388	-352	-732	-710	-352
-178	8855	339	-178	-5231	171	-178	-4166	61	.178	.3763	102	-178	-3997	296	-178	- 3765	0/11.	091-	542	-178	-5742	114	-178	.5562	-205	-178	-12187	.543	-178	.7742	-1401	9.1.	.12266	D 0	.12297	2057	-178	-12297	-2008	178	- 5975	-3238	-178	-5932	.3215	-178	-4036	-3121	-178
919	-11047	.1912	979	-11090	- 1913	979	-11089	793	919	-11076	270	616	-11091	337	979	-11007	20 0	7	1281	616	-10434	.1550	919	-10679	1001			-2038	919	-11237	-3065		_	90 0			979		-2103	919	-11309	-2080	919	-11283	149	919	11256	249	979
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1 2 2 1		:	30	-12	1568	-12		1745	-12		1141.	31	-2082	-12	00	-12		-494	-12		1532	13		1489	•	211	-12		-139	-12	.3050	-12		-890	-12	,	8/9-	71	334	-12		-1324	-12	;	67
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212			1318	-73	-159	-73		830	-73	346	הלי	•	1043	.73	2358	-73		3002	-73		1494	- 73	; י	.73	•	3079	-73		3027	.73	-1615	-73		1211	-73	1600		?	2890 .	-73		2959	-73		
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. 463	.130		-864	.130	-302	.130		105	.130	3,5	.130		-684	-130	-660	-130		878	-130	;	582	-130	3 6 1 6	.130		437	-130		•	-130	-630 .	-130		'	-130	. 1191		,	•	-130		-516	-130	916	
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. 1595	205	-23	-2438	206	-441	206	-24	1191-	706	-1231	206	-24	-1538	206	305	206		-1578			מחם	907	.1313	206		-623			-679					-571			206		366	206		-1376	-116		i i
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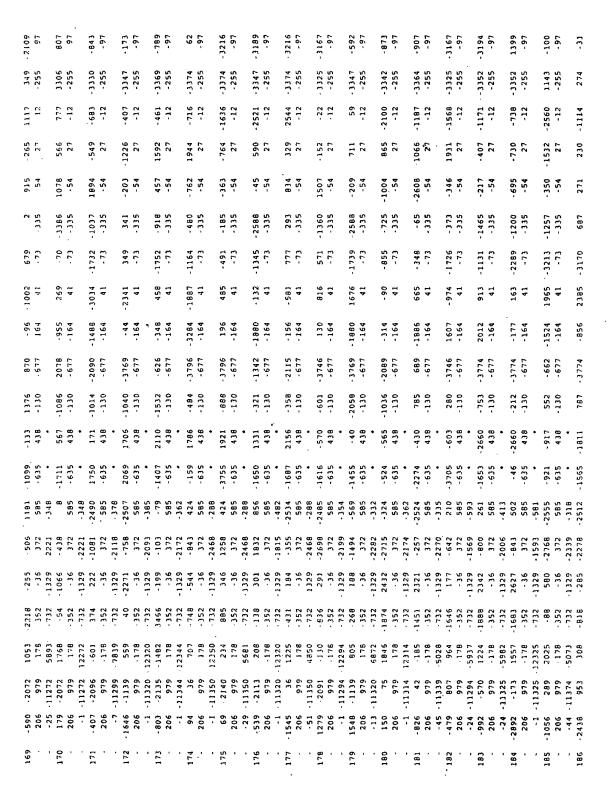
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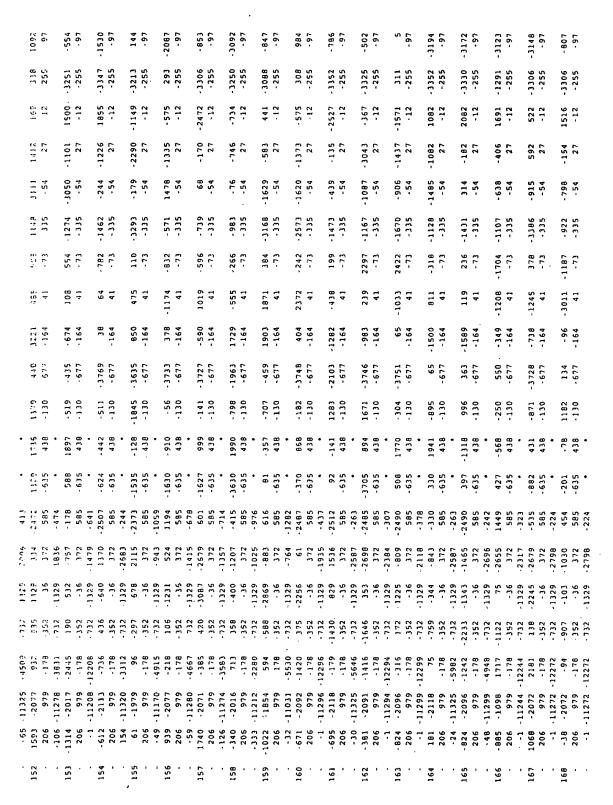
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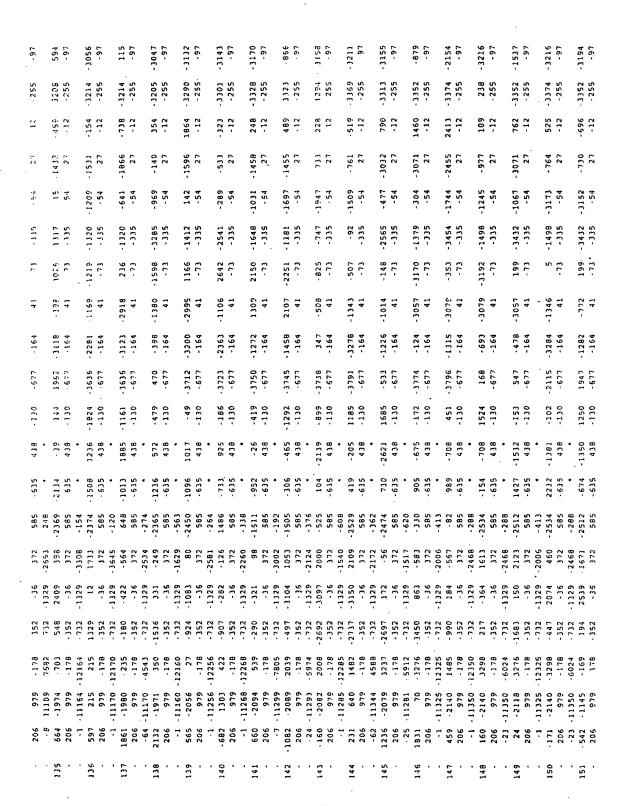
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255	•	3299	255		-3327	557.	307	-255		-3342	-255		2061	-255	15.4	-255		248	-255		-3314	.255		-3320	.255		-3320	567-	315	-255		1398	-255	523	-255	!	1266	-255	1		567-	1812	-255			-255
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7.7		130	7.5		.550	7	-1439	27		-575	. 27		185	27	805.	27		-23	27		1709	27		-587	27	;	83	· ·	-2409	27		-1590	77	-2914	27		-899	27		-1333	7	.577	27		- 85	27
ņ		37.0	.54		122	, ,	-1875	-54		-3141	. 54		748	-54	4984	- 54		559	-54		-87	- 54		.494	-54.	,	196-	ń	-757	- 54		66.	40.	-1492	-54		516	-54	;	1 B C	* n	468	.54		108	-54
135		17.	+315		.1245	crr.	-1433	-335		-145	-335		-655	-335	.18	-335		151	.335		646	-335		1779	-335		1955		908	-335		-1051	crr.	-1972	-335		-1988	-335	į	P/9-	000	-1316	,335		-1313	-335
. 7.1		e c t	7.3		. 1099. 		.833	.73		-1247	-73		-3155	-73	343	-73		-31	-73		556	-73		379	٤٢٠	;	22 -	-	546	-73		2339	۲,۰	2477	-73		-29	-73	:		?	-3069	-73		-3064	-73
7		36.7	7	;	. 193	7	1575	41		2100	‡		828	41	-273	41		7.3	41		-352	41		-550	41		6/71	;	-814	41		-987	,	-712	41		-2928	4		CC 6 2 -	;	-2955	41		- 2950	4.1
1.51		1212	.154		1250	5 01	403	-164		-1009	. 164		-3247	-164	.62	-164		-133	. 164		-434	-164		-3229	-164		-3229		-1242	-164		-3144	* O T -	-812	-164		-1092	-164		164	5	-1133	-164		-319	-164
577		\$20	677	:	-3749	- p	1560	-611		-2089	-677		.2082	-611	.3718	-677		-1330	-677		-3736	-677		996-	.617		-552		-3741	-677	;	295-	0	-2015	-677		-144	-677	,,,,	7,79		-3673	-677		-3668	-677
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438	•	1592	438	• ;	\$6.45.		-1319	438	•	-2650	438	•	-1340	438	.1068	438	•	-1801	438	•	-2622	438	•	-1097	438	• 5	438	•	42	438	• ;	94.	D •	-807	438	•	-375	438	0101	478	•	-1210	438	•	-2553	438
.635	٠	505	. 635	•	96/.	•	.1429	-635	٠	-2814	-635	•	-1371	.635	-898	-635	•	-1396	-635	•	-3692	-635	•	-3700	.635		6.63	•	.81	-635	• ;	1//1	•	-628	-635	٠	-1030	-635	. 167	-635		-3631	-635	•	.3626	-635
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.36	.1329	-585	-36	1329	3106	-1329	1176	-35	.1329	375	.36	.1329	.3118	96-	644	- 36	.1329	160	-36	-1329	-286	- 36	-1329	814	- 36	6261	- 36	-1329	1392	-36	1329	996.	-1329	2257	- 36	-1329	2520	95.	1900	-36	-1329	2875	-36	-1329	-524	-36
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3256	.255	,	. 3202))	-3296	-255		-3320	.255		315	-255	:	2161-	667	313	-255		-3251	-255	;	980	-255		-3224	667 .		1626-	567.	4111	-255		-2917	-255	0186.	.255		-3080	-255		-3223	-255	į	575	-255		-3314
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1101	2,3	ć	, , , , ,	:	- 928	7.7		1060	۲2		-507	23		- 1404 - 1404	,	-993	27		٠7.	27	;	.535	27	į	169	7		507.	7	-1020	27		-862	72	. 3540	27		-2134	27		• 900	72		-814	72		153
1370	7.	;	5191.	ζ.	1115	-54		-62	-54		-96-	- 54	:	133	, n	-828	- 54		-1364	-54		23	- 54	ì	-565	-54	,	, 771	- 54	1836	-54		111	-54	2020	4.	,	916	-54		-139	-54		-628	-54		-625
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06	7	;	.1103	;	-1561	41		-2318	41		905-	4		1301	7	-3029	41		-536	4,		343	47	9	-725	4	ć		41	.170	41		-284	‡	410,	41		-187	41		-138	41		-459	41		-1489
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3353	352	. 732	167	-732	3393	352	. 732	-1643	-382	-732	.371	-352	.732	9.55	252.	607	-352	-732	1631	-352	-732	128	-352	-732	-1091	-352	-732	1917	.352	20.00	- 352	-732	-1363	-352	26/-	כיי.	.732	-2419	-352	-732	.2590	-382	.732	-1706	.352	.732	7
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-42	ەر ق	.11215	-1968	-11152	-2062	_	_	446	919						6/6	107	979	-11294	-1074	979	.11208	1990	ó.6	-11117	-1990	979	751111.	1997	979	5005	979	-11086	-639	626	25801-	000			919	-11022	-1989	979	11182	-1141	979	11333	-2080
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	199		-3116	- 97		2673	- 97		3232	.97		1585	- 97		-2586	- 97		909-	- 97		66	. 66		. 3197	í.ó		3215	.97		-2142	- 97		-941	- 97	-3147	-97		-2101	- 97		-862	-97		-578	-97		-743	-97
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	1303	'n	1328	.54		1881	-54		-830	-54		126	-54		74	.54		-118	-54		- 366	.54		1092	54		-150	-54		220	-54		1516	- 54	-833	-54		-1717	-54		-1693	-54		-415	-54		-3055	-54
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	150	-130	.1036	-130		-80	-130		-1322	-130		σ.	-130		-140	-130		-862	-130		-949	-130		-669	-130		-1517	-130		-1794	-130	į	4 / 1	061.	1413	-130		-1042	-130		-137	-130		1116	-130	į	.373	-130
•	-503	4 38	-1044	438	•	-2550	438	•	-2382	438	•	-889	438	•	352	438	•	646	438	•	- 704	438	•	80	438	•	615	438	•	-113	438	• :	014	D *	-444	438	•	-2144	438	•	-2138	438	•	306	438	•	-405	e.
•	63	ردو. د	256	-635	•	-1534	-635	•	.670	-635	•	-2066	-635	٠	-908	-635	•	-3348	-635	•	.706	-635	•	B69·	.635	•	7	.635	•	-61	-635	• 6	909.	n *	-1360	-635	•	1859	-635	•	2011	-635	•	-107	-635	•	-3637	.635
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-5574																																																5817
-11141	1956	-11149	.2040	979	-11236	. 59	919	- 11202	-811	616	11016	.1478	919	-10589	.1510	979	-10628	.1734	979	-10893	-2040	616	-11239	555	616	-11329	430	979	-11351	15	7. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	16511-	979	.11206	819	979	-11274	6.0	979	-11304	20	979	-11291	-2093	979	-11297	2207.	-11215
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- 64	-30	585	.78	-24	585	-77	0	585	-74	65	585	99-	199	585	-64	249	585	-61	303	•	•	
-4148	-243	372	-4251	-237	372	-4274	-213	372	-4319	-148	372	-4478	- 14	372	-4535	36	372	-4604	90	•	•	
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-7341	364	919	-7251	370	979	-7235	394	616	-7154	459	979	-6982	593	919	-6474	644	979	-6305	697	•	•	
-103	-410	206	-33	-403	206	-86	-379	206	-210	-314	206	-402	-180	206	-212	381	206	-170	-76	•	•	
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-834	-185	504	-12	47	-12		-834	-12	776	, c	•	859	-12		- 55	-12		-505	-12		-697	-12		1473	-12		-94	-12		1020	-12		92	-12		1847	-12
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25	-1056	-1056	-54	ננט	.54		137	-54	,	# 0 T :	÷n.	-947	-54		606-	-54		-52	- 54		-480	-54		-864	-54		-273	-54		208	-54		-239	-54		-372	.54
-1337	-1337	-1337	-335	7551-	-335		-1337	-335	6	מאבן.	C C C -	-418	-335		-929	-335		-1190	-335		-1190	-335		-1145	-335		-1145	-335		-1132	-335		-838	-335		-199	-335
679 -73	129	2701-	-73	נפונ	-73		-188	-73	1	6/6	٤/٠	-282	-73		2454	-73		265	-73		-355	-73		-883	-73		106	- 73		-870	-73		-844	-73		Н	-73
323 41	.269	-405	41	. 963	41		- 962	41	6	976	7	3.5	41		171	41		-814	41		828	41		-770	41		893	41		292	41		1798	41		24	41
550	.519	3636	-164	1166	-164		-1166	-164	6	950T-	- 104	-1058	-164		-1019	-164		-1019	-164		-1019	-164		-975	-164		746	-164		-961	-164		-935	-164		-810	-164
827	-1679	1182	-677	00.00	- 677		4 9 4	-677	•	0/51-	, , ,	-1570	-677		88	-677		-1531	-677		-1531	-677		-1487	-677		-1487	-677		-1473	-677		-1447	-677		-1323	-677
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· \$64 438	539 438	1186	438	• 90	438	•	427	438	• ;	- 4 5 to	4. 5.	779	438	•	-417	438	•	755	438	*	-49	438	*	1707	438	•	99	438	•	-359	438	•	-333	438	•	-208	438
-1637	-1057	4 4 7 7 7 1 7 1	-635	* '	7591,	•	-1637	-635	* 6	-1529	ردو- د +	.1529	-635	•	-919	-635	•	-448	-635	*	-311	-635	*	-998	-635	*	-1446	-635	•	-1432	-635	*	-1406	-635	*	-778	-635
585	-116 -417 585	-116	585	-116	582	-116	-417	585	×116	805-	285	- 308	585	-106	-270	585	-102	-270	585	-102	-270	585	-102	-225	585	- 96	-225	585	96-	-212	585	-93	-186	585	-91	-61	585
-630	-3696 -630 372	-3696	372	-3696	372	-3696	-630	372	-3696	175-	312	.521	372	-3825	-483	372	-3876	-483	372	-3876	- 50	372	-3876	-438	372	-3960	-235	372	-3960	-425	372	-3996	-399	372	-4034	-274	372
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.385	-9205 -439 -178	-9205	-178	-9205	-1101	-9205	-187	-178	-2913	-1072	-1/8	2,70-	-4.78	-4185	-1033	-178	-8883	-1033	.178	-8883	-1033	-178	-3915	-989	-178	-8775	- 989	- 178	-5378	-363	-178	-4564	- 949	-178	-2545	-825	-178
1857	-8205 754 979	-8205	979	-8205	979	-8205	2846	979	-8205	1662	616	1161	979	-7972	1019	979	-7883	2054	979	-7883	125	919	-7883	2183	979	-7775	1556	919	-7775	3140	979	-7738	1100	979	-7670	333	979
-315	- 7 444 206	7-	206	r-,	206	-7	- 196	506	-211	- 482	206	4 4 4	206	- 88	461	206	9	46	206	6,	1236	206	-106	-195	206	-10	-605	902	-42	-101	206	-69	-565	206	-280	-440	206
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438	•	613	438	•	1275	438	•	368	438	٠	-765	438	•	15	438	*	1501	438	*	58	438	•	4	438	*	732	438	•	954	438	•	87	438	•	70	438	*	-158	438	*	1021	438	•
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	64	£91.		600	-164		-1310	-164		65	- 164		558	-164		-1310	-164		1178	-164		57	-164		234	-164		-136	-164		-925	-164		-1367	-164		-1367	-164		-1367	-164		78
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•	329	438	•	1383	438	•	106	438	•	-35	438	٠	141	438	•	447	438	*	-429	438	*	829	438	•	794	438	•	695	438	•	-47	438	•	67	438	*	-34	438	•	-122	438	•	711
•	-857	-635	•	-1748	-635	٠	-1781	-635	•	-1781	-635	•	-1781	-635	*	-1781	-635	٠	-1781	-635	• .	-1781	-635	•	-1781	-635	•	-1781	-635	•	-1838	-635	•	-650	-635	•	-1838	-635	*	-1838	-635	•	-1529
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216	. 255		-1340	-255		1608	-255		-1349	-255		-1349	-255		314	-255		2911	-255		-1330	. 255		-1352	-255		-1370	-255		-1370	-255		-1370	-255		1263	-255		-1370	-255		1119	-255
٠ 4	-12		-507	-12		-811	-12		-528	-12		- 765	-12		181	-12		341	-12		9	-12		79	-12		-124	-12		-245	-12		- 26	-12		1460	-12		-135	-12		-121	-12
42	27		45	27		680	27		302	27		595	27		285	27		904	27		-732	27		569	72		992	27		1105	27		801	27		-11	27		882	27		-893	27
לבי	3.0		462	-54		80	-54		281	-54		753	-54		1277	-54		970	-54		711	- 54		542	- 54		1417	-54		1585	-54		892	-54		419	-54		138	-54		1616	-54
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759	, E	•	270	-73		821	-73		4	-73		692	-73		-1167	- 73		255	-73		-300	-73		361	-73		-890	-73		-1188	-73		284	-73		-442	-73		158	-73		-517	-73
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.16	1329	.1711	- 35	-1329	.918	-36	.1329	.848	-36	.1329	-1447	.36	-1329	.958	-36	-1329	- 796	-36	-1329	.520	
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112	316		678	-335		- 2678	-335		-810	-335		829	-335	,	310	1	406	-335		-868	-335		349	-335	!	245	-335	;	-423	- 335	2	- 135		566	-335	,	996	-335	;	838	-335	,	597	- 335	000	000	-335
86.07	- -		190	-73		29B	57.		557	-73	•	780	-73	;	73		760	.73		882	.73		636	.73		862	.73		1020	- 73	173		•	636	-73		1531	-73		1090	.73		1951	-73	1011	7071	۲ <u>-</u>
3₽9	7		200	41		-413	\$		605	41		1139	41	ć	ر او . د د د	;	478	41		- 953	41		.163	41		-98	41		- 529	41	u o	5.4	!	-561	41		209	41		-277	4	;	-2394	,41	,	P667-	41
1258	1.51		.1739	-164		. 887	.164		454	-164		725	-164	;	106.	*01-	- 1858	-164		-1348	-164		-2538	-164		.1923	.164		-2520	-164	,	2002-	·	-687	-164		-2599	-164		-1081	-164	;	417	- 164	:	7/5-	-164
1996			.1862	.677		-3020	-677		-3051	-611		443	-611		4 (.1005	.677		-3033	-677		-3050	-677		-3012	-677		137	-611	,			354	-677		-2917	-677		-3111	-617		-145	-677	:	- 1111	-677
ć.			-469	-130		986	-130		~	-130		-175	-130		-1018	130	-	-130		672	-130		979	-130		615	-130		- 222	-130	•	. יי פני	3	96	-130		905	-130		903	-130	;	383	-130	,	695	-130
§1 6	438	•	- 581	438	•	135	438	•	-1936	438	•	-219	438	•	6 4 9	n •	119-	438	•	-519	438	•	-1156	438	٠	4	438	•	- 967	438	• L	C 7 .	*	263	438	•	41	438	•	-1092	438	•	-869	438	• ;	192	438
1214	6.35	•	- 963	-635	•	954	-635	•	942	-635	•	-479	-635	•	27	. 64.	919	-635	٠	294	.635	•	2	-635	•	226	-635	•	- 194	-635	• !	, 44	•	-86	-635	•	-2479	-635	•	767	-635	•	-804	-635	• (.3070	-635
422	20.2	. 210	.1788	585	-207	-1758	585	-275	- 36	585	-256	-1785	585	-239	1225	2.6	776-	. 6	.317	9	585	-247	185	585	.116	- 59	285	.165	.353	585	-242	0771	.248	265	585	-134	-283	585	-134	-661	585	-134	414	585	.134	·Sı	585
41,4		. 2887	. 954	372	-2901	.834	372	.2527	-1234	372	-2619	-692	372	-2710	47	3/5	C + C 2 -	172	-2342	-1985	372	-2667	-604	372	.3697	- 503	372	.3212	- 560	372	-2695	108-	-2661	.1273	372	-3499	-2062	372	-3499	-2062	372	-3499	-627	372	-3499	. 2062	372
. 23	: :	2711.	. 597	-36	.1329	461	-36	.1329	-1851	-36	-1329	- 156	-36	-1329	630	36.	5751-	35.	-1329	476	-36	-1329	305	-36	-1329	265	-36	-1329	-809	-36	-1329	11.59	-1329	172-	- 36	-1329	-1030	-36	.1329	-1172	-36	-1329	-604	- 36	-1329	1187	- 36
et.		, ,	8.5 B	.352	- 732	536	-352	-732	-163	-352	-732	-224	-352	.732	479	-352	75/.	152	.732	. 17.	.352	-732	-192	-352	.732	-552	- 352	-732	899	-352	-732	٠. در در د	-732	-1975	- 352	- 732	-924	-325	-732	-1238	-352	-732	-152	-352	732	52	-352
511		4750	1345	-178	-4354	623	-178	.5599	1029	.178	4638	634	.178	-4445	549	.178	2 0 0	178	.4366	1527	.178	-5578	-438	-178	-4984	739	.178	11447	816	-178	11471	613	11521	-492	.178	11565	131	-178	11565	-660	.178	11565	-862	-178	11565	-785	-178
11417				979																																			•			•			•		
12.1				506																																											
00	. 7		ç	,	,	31			32			33		•	34	,	٠ ;	ç	٠.	36			3.7			38		•	39		•	40		41			42			43		ı	4			45	•

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```
wdef(cpp32,protein,'CPP32').
wdef(crkl, protein, 'CrkL').
wdef(ctf, substance, 'COOH-terminal fragment').
wdef(cytokine, smallmolecule, cytokine).
wdef(cytosol, structure, cytosol).
wdef(djnk,protein, 'DJNK').
wdef(djun, protein, 'DJun').
wdef (dynamitin, protein, dynamitin).
wdef(erk, protein, 'ERK').
wdef(eto,smallmolecule,'ETO').
wdef(etoposide, smallmolecule, etoposide).
wdef(fad, disease, 'familial Alzheimer'''s disease').
wdef(fyn, protein, 'Fyn').
wdef(gdp, smallmolecule, 'GDP').
wdef (gelsolin, protein, gelsolin).
wdef(gp120,protein,'gp120').
wdef(grb2, protein, 'Grb2').
wdef(gst, protein, 'glutathione S-transferase').
wdef(gtp, smallmolecule,'GTP').
wdef(hsp70,protein,'HSP70').
wdef(human, species, human).
wdef(ikk, protein, 'IKK').
wdef(inactivated, state, inactive).
wdef(inactive, state, inactive).
wdef(jnk, protein, 'JNK').
wdef(jnk, protein, 'JNK').
wdef(jnk2, protein, 'JNK2').
wdef(kap3, protein, kap3).
wdef(kdakt, protein, 'KDAkt').
wdef(kinase, protein, kinase).
wdef(kinectin, protein, kinectin).
wdef(klc,protein,klc).
wdef(lamin, protein, lamin).
wdef(myosins,protein,myosins).
wdef(nmdar,protein, 'NMDAR').
wdef(nmdar2b, protein, 'NMDAR2B').
wdef(ntf, substance, 'NH2-terminal fragment').
wdef(p70s6k, protein, p70s6k).
wdef(p78s6k, protein, p78s6k).
wdef(parp,protein, 'poly(ADP-ribose)polymerase').
wdef(pdkl, protein, 'PDKl').
wdef (peptides, protein, peptide).
wdef(pkb, protein, 'PKB').
```

```
phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7-1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex,[t,'-',cell,receptor],'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'-',cell,antigen,receptor],'T-cell antigen red
eptor',r).
phrase(threonine, aminoacid, [threonine, 229], 'threonine 229', r)
phrase(transcription, protein, [transcription, factor], 'transcript
ion factor',r).
phrase(trypan, smallmolecule, 'trypan blue', r).
phrase(wt, protein, [wt, akt], 'WT Akt',r).
phrase(zap, protein, [zap, '-', 70], 'ZAP-70', r).
phrase(zdevd, smallmolecule, [zdevd, '-', fmk], 'zDEVD-fmk', r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin, protein, actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad, disease, 'Alzheimer''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef (anergic, state, inactive).
wdef (anergic, state, inactive).
wdef (anergy, state, inactive).
wdef(antibody,complex,antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef (apoptosis, process, apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase, protein, caspase).
wdef(caspase, protein, caspase).
wdef(cbl, protein, 'Cbl').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol, smallmolecule, cholesterol).
```

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phosphorylate, r). phrase (phosphatidylinositol, smallmolecule, [phosphatidylinositol, 1 ,',',4,',',5,'-',triphosphate], 'phosphatidylinositol 1,4,5-tripho sphate',r). phrase (phosphoinositide, protein, [phosphoinositide, '-', dependent, protein, kinase], 'PDK1',r). phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip ase C-1', r). phrase(poly,protein,[poly,'(',adp,'-',ribose,')',polymerase],'poly (ADP-ribose) polymerase',r). phrase(polyvinylidene, structure, [polyvinylidene, difluoride, memb ranes], 'polyvinylidene difluoride membranes', r). phrase (presenilin, protein, [presenilin, 1], 'presenilin 1', r). phrase (presenilin, protein, [presenilin, 2], 'presenilin, 2', r). phrase (productively, state, [productively, stimulated], active, r). phrase (protein, protein, [protein, tyrosine, kinase], 'protein tyrosi ne kinase', r). phrase (protein, protein, [protein, kinase, c], 'protein kinase C', r). phrase(ps2, substance, [ps2, '-',ctf], 'presenilin 2 COOH-terminal fra phrase (ps2, substance, [ps2, cleavage, fragment], 'presenilin 2 cleava ge fragment', r). phrase(pvdf, structure, [pvdf, membranes], 'polyvinylidene difluori de membranes', r). phrase(raf, protein, [raf,'-',1], 'Raf-1', r). phrase(raf,protein,[raf,'-',1], 'Raf-1',r). phrase(rap1,complex,[rap1,'-',gtp], 'Rap1-GTP',r). phrase (requirement, need2, [requirement, for], need, r). phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r). phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r). phrase(serine, substance, [serine, residues], 'serine residues', r phrase(src, domain, [src, homology, 2], 'Src homology 2',r). phrase(src, domain, [src, homology, 3], 'Src homology 3',r). phrase(srebp,protein,[srebp,'-',1], 'sterol-regulatory element bin ding protein 1',r). phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin ding protein 2',r). phrase (sterol, protein, [sterol, '-', regulatory, element, binding, prote in,1],'sterol-regulatory element binding protein 1',r).

phrase (sterol, protein, [sterol, '-', regulatory, element, binding, prote

in,2],'sterol-regulatory element binding protein 2',r).

```
phrase(ice, protein, [ice, '/', ced, '-', 3], 'ICE/Ced-3', r).
phrase(il, gene, [il,'-',2,gene], 'gene encoding interleukin-2', r
) .
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in, state, [in, the, anergic, state], inactive, r).
phrase(inducible, cell, [inducible, h4, cell], 'inducible H4 cell', r
) .
phrase(interleukin, protein, [interleukin, '-', 2], r).
phrase(interleukin, protein,[interleukin, '-', 3], 'interleukin-3
',r).
phrase(interleukin, protein, [interleukin, '-', 1, beta, converting, enzy
me], 'interleukin-1 beta converting enzyme',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, [jurkat, cells], 'Jurkat cell', r).
phrase(kif3a, protein, [kif3a, '/', 3, b], 'KIF3A/3B', r).
phrase(lbl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cells',r).
phrase(lbl,cell,[lbl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let,'-',23], 'Let-23', r).
phrase(may, probability, [may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3E',r).
phrase(myc, protein, [myc, '-', pdk1], 'Myc-PDK1',r).
phrase(myc,protein,[myc,'-',p70s6k],'Myc-p70s6k',r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r)
phrase(myr, protein, [myr, '-', akt], 'Myr-Akt', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate, receptor], 'N
MDAR', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate], 'NMDA').
phrase(native, cell, [native, h4, cell], 'native H4 cell', r).
phrase(nf, protein, [nf,'-','[',kappa,']',b], 'NF-[kappa]B',r).
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2, substance, [nh2, '-', terminal, fragment], 'NH2-terminal fr
agment', r).
phrase(nih, cell, [nih, '-',3,t3,fibroblasts], 'NIH-3T3 fibroblasts'
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
phrase(normal,substance,[normal,ntf],'normal NTF',r).
phrase(nuclear, protein, [nuclear, factor, kappa, b], 'NF-[kappa]B'
phrase(p150Glued, protein, [p150Glued, -, arp1], 'p150Glued-Arp1', r).
```

phrase(phosphate,phosphorylate2, [phosphate, incorporated, into],

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```
phrase(caspase,protein,[caspase,'-',6],'caspase-6',r).
phrase(caspase, protein, [caspase, '-', 7], 'caspase-7', r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
phrase(cleavage, site, [cleavage, site], 'cleavage site', r).
phrase(cleavage, substance, [cleavage, products], 'cleavage products',
phrase(cooh, substance, [cooh, '-', terminal, fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crkl, complex,[crkl,'-',c3g,complex],'crkl-c3g complex',r).
phrase(dcp,protein,[dcp,-,1],'DCP-1',r).
phrase(did, negation, [did, not], not, r).
phrase(ebv, species, 'Epstein-Barr virus', r).
phrase (epstein, species, [epstein, '-', barr, virus], 'Epstein-Barr vi
rus',r).
phrase(familial, disease, [familial, alzheimer, '''', s, disease], 'famil
ial Alzheimer'''s disease',r).
phrase(gene, gene, [gene, encoding, interleukin, '-', 2], 'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r).
phrase(gtp, complex,[gtp,exchange,of,rap1], 'GTP exchange of Rap1',
r).
phrase (guanidine, protein, [guanidine, nucleotide, '-', releasing, fac
tor, c3g], 'guanidine nucleotide-releasing factor C3G1,r).
phrase (guanidine, smallmolecule, [guanidine, nucleotide], 'guanidine
nucleotide',r).
phrase(guanosine, smallmolecule,[guanosine,triphosphate],'guanosin
e triphosphate',r).
phrase (guanosine, smallmolecule, [guanosine, diphosphate], 'guanosine
diphosphate',r).
phrase(h4,cell,[h4,cell,line], 'H4 cell line',r).
phrase(h4,cell,[h4,human,neuroglioma,cells], 'H4,human,neuroglioma
,cells',r).
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb],'HA-[Delta]PHPK
B',r).
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,']'],
                                                               'I[ka
ppa] B - [beta] ', r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'],
pa]B-[alpha]',r).
phrase(i,protein, [i, '[',kappa, ']',b], 'I[kappa]B',r).
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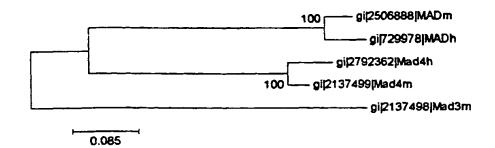
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% lexsemsub.pat
% revised March 17, 2000
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:-multifile(wdef/3).
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BAA', r). % ?
phrase('[',smallmolecule, ['[',zeta,']',1, subunit], '[zeta]1 subu
nit', r). %?
phrase(116, protein, [116, '-', kd, fyn, '-', associated, protein], '116-k
D Fyn-associated protein',r).
phrase(116, protein,[116,'-',kd,protein], '116-kd protein',r).
phrase(3,protein, [3,'~',kinase,'-',akt], '3-kinase-Akt',r).
phrase(ability, affirmation, [ability, to], [], r).
phrase(agc, protein, [agc, protein, kinases], 'AGC', r).
phrase(akt,protein, [akt, mutant], 'Akt mutant', r).
phrase(alternative, substance, [alternative, ntf], 'alternative NTF', r
phrase (antibody, protein, [antibody, to, phosphotyrosine], 'anti-phosp
hotyrosine',r). .
phrase (antigen, complex, [antigen, receptor], 'antigen receptor', r).
phrase (ap, protein, [ap, '-', 1], 'AP-1', r).
phrase (aspargine, site, [aspargine, '-', 141], 'aspargine-141', r).
phrase(b, cell, [b,cell], 'B cell', r).
phrase(b, cell, [b,cells], 'B cell', r).
phrase(b, species,[b,lymphoblastoid,cells], 'B lymphoblastoid cell
phrase(b,cell,[b,lymphoblastoid,cells], 'B lymphoblastoid cells',r
phrase(b7, protein, [b7,'-','1'], 'B7-1',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV', r).
phrase(casp, protein, [casp, '-', 3], 'caspase-3', r).
phrase(caspase, protein, [caspase, '-', 3, family, protease], 'caspase-3
 family protease',r).
phrase(caspase, protein, [caspase, '-', 3, precursor], 'caspase-3 precur
phrase(caspase, protein, [caspase, '-', 3], 'caspase-3', r).
phrase(caspase, protein, [caspase, -, 3], 'caspase-3', r).
```

Appendix A

Page 1

A.



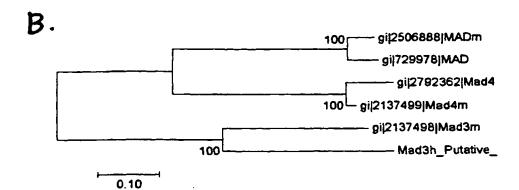


Figure 18. A-B

C

>Mad3b(Putative)

MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLK RCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLKERLRTKQQSLQRXWMQLRGLAGAAERER LRADSLDSSGLSSERSDSDOEELEVDVESLVFGGEAELLRGFVAGOEHSYSHVGGAWL

D

	MANAGEMENT IN TRANSPORT STREET VARIABLE STREET VARIABLE STREET
gi12506888[MADE	MATAVOHNIQLLLEAD/VERREALEHGYASHLPYS-KORDAFKRRIKKPKKISTSSRSTHKEHEKKRRAHLRLCLEKLIGLVPLGPESSRHTTLSL
gi 17299781MADh	PAAAVRINI OILLEAADVLERREREAEHOYASKLPYIOKOROALKRAIKSKKINS ==5 SRS THNEHEKURAAHLRLCLEKLKGLVPLGPESSRHTTLSL
g1127923621Med4h	melmsll: lleaafyleradreaehgyasvlpfdgdfarenykaaglvrkap mnrs shnelekhrraklrlyleglkglvplgpdstrhttlsl
gi121374991Med4m	meinslill learey lerrdreaehgyashipfdgdfarkytaglvrkgp mnrs shheleknrraklriyleolkolgfigfdstrhttis li
gi 2137498(Mad3m	-nepvashi ovllgaaefilerrereaergyas lophhspgtvorrrkpplgadgalrsgrs vhnelekrrraqlkrgleglrggmplgvdotryttis li
Med3h Putative	-neplasnig/llgaaeflerrereaehgyaslophrspgpihrrkkrpppapgadsgrsvhnelekrrraqlkrclerlkgg1f2ggdcaryttlsll
gi125068881MADm	tkaklhikkledcorkavhoidoloregrhikrriekigaertrhdsvg-svvssersdsdreeldvdvdvdvdvdvdvgtdylkgdlghsss-
gi17299781HADb	tkaklhikkled@rkavhoidoloreorhikrolekigierirhdsig-stvssersdsdreeidvdvestdyltgdldwssss
gi127923621Mad4h	Krak/Hikkleeqdrralsikeqloqehrflkrrleqlsvqsvirvrtdstg-savstddseqevdieghefgpgeldsvgs-
gi (2137499 (Mad4m	K-akchikkleeodrralsikeolorehrfikrrleolsvosvrvatdstg-savstddseoevdiegreforgeldsags-
q1121374981Med3m	R-ARVHIGKLEEGEGGARALKEKLRSKOOSLOOOLEGLOGLPGARERERLRADSLDSSGLSSERSDSDGEDLEVDVENLVFG-TETELLOSF
Med3h Putative	rraphie okledoforarolnerlikkooslork-nolkglagaaferlikadslossglssersdsdoeEle-dveslvfg-geaellikgf
gi125068881HADb	vsdsdergshoslg-sdegyssat-kraklodgheaglg:
g 119 299781 M ADh	vsdsdergsmgslg-sdegysstsfmriklgdsbokcig:
gi12792362 Mad4b	SSDADDHYSLQSGTGGDSGFGPHCRRLGRPALS
g1 2137499 Hadts	SSDADDHYSLOS SGCSDSS YGHPCRLPGCPGLS
q1121374981Mad3m	SAGREHSYSRSTCAWL
Med3h Putative	VAGOERSYS RVGGAWL

Figure 17 C-D

BASE COUN	T 130	a 234 c	258 g	106 t	5 others
ORIGIN					
1	cagccgcttg	ctccggccgg	caccctaggc	cgcagtccgc	caggetgteg cegacatgga
61	acccttggcc	: agcaacatcc	aggtcctgct	gcaggcggcc	gagttcctgg agcgccgtga
121	gagagaggco	gagcatggtt	atgcgtccct	gtgcccgcat	cgcagtccag gccccatcca
181	caggaggaag	aagcgacccc	cccaggctcc	tggcgcgcag	gacageggge ggteagtgea
241	caatgaactg	gagaagcgca	ggagggccca	gttgaagcgg	tgcctggagc ggctgaagca
					ctgagcctgc tgcgccgtgc
					gcccgacagc tcaaggagag
421	gctgcgcaca	aagcagcaga	gcctgcagcg	gcantggatg	cagctccggg ggctggcagg
					tcctcaggcc tctcctctga
541	gcgctcagac	tcagaccaag	aggagctgga	ggtggatgtg	gagageetgg tgtttggggg
					cacagctact cgcacgtcgg
					tgccctctta ctcgttgccc
	aagcccactt				

Figure 17B

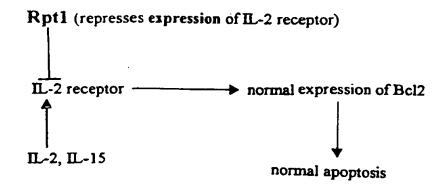
TBLASTK 2.0.6 [Jan-05-1999]

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Query- g1121374981Mad3m (205 letters) gb:AA278224:AA278224 zs77e05.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703520 5' similar to TR:G1184157 G1184157 MAX-INTERACTING TRANSCRIPTIONAL REPRESSOR.; Length = 430 Score = 209 bits (526), Expect = 1e-53 Identities = 104/124 (83%), Positives = 116/124 (92%), Gaps = 1/124 (0%) Frame - +2 MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRS 60 Ouery: 1 MEP+ASNIQVLLQAAEFLERREREAEHGYASLCPH SPG + RR+K P QAPGA +SGRS Sbjct: 56 MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRS 235 Query: 61 VHNELEKRRRAQLKRCLEQLRQQMPLGVDCTRYTTLSLL-RARVHIQKLEEQEQQARRLK 119 VHNELEKRRRAQLKRCLE+L+QQMPLG DC RYTTLSLL RAR+HIQKLE+QEQ+AR+LK Sbjct: 236 VHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLK 415 Query: 120 EKLRS 124 E+LR+ Sb1ct: 416 ERLRT 430 dbj[C02407[C02407 HUMGS0012279, Human Gene Signature, 3'-directed cDNA sequence. Length = 348 Score = 97.5 bits (239), Expect = 6e-20 Identities = 51/63 (80%), Positives = 56/63 (87%) Frame - +3 Query: 125 KQQSLQQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQEDLEVDVENLVFGTETE 184 QL+GL GA ERERLRADSLDSSGLSSERSDSDQE+LEVDVE+LVFG E E KQQSLQ+ SDJct: 45 KQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAE 224

Figure 17 A

Query: 185 LLQ 187 LL+ Sbjct: 225 LLR 233

Activated CD4⁺ T-cells



When rpt1 is knocked out:

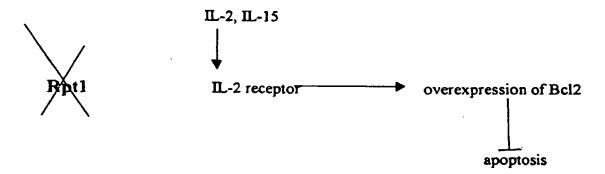


Figure 16

>sp|P15533|RPT1_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-1r [Mus musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15

10 15 20 25 30

1 S R S X Q K F F Q E L S K S L D A F P E D F C R H K V L P Q

31 L L T A F E F G N A G A V V L T P L F K V G K F L S A E E Y

61 Q Q K I I P V V V K M F S S T D R A M R I R L L Q Q M E Q F

91 I Q Y L D E P T V N T Q I F P H V V H G F L D T N P A I R E

121 Q T V K S M L L L A P K L N E A N L N V E L M K H F A R L Q

151 A K D E Q G P I R C N T T V C L G K I G S Y L S A S T R H R

181 V L T S A F S R A T R D P F A P S R V A G V L G F A A T H N

211 L Y S M N D C A Q K I L P V L C G L T V D P E K S V R D Q A

241 F K A X R S F L S K L E S V S E D P T Q L E E V E K D V H A

271 A S S P G M G G A A A S W A G W A

Figure 14D

BASE	COUNT	405	а 545 с	493 g	278 t	6 others						
ORIGIN												
	1	cagccgaagc	amgcaaaaat	tcttccagga	gctgagcaag.	agcctggacg	cattccctga					
			cggcacaagg									
	121	tggggccgtt	gtcctcacgc	ccctcttcaa	ggtgggcaag	ttcctgagcg	ctgaggagta					
	181	tcagcagaag	atcatccctg'	tggtggtcaa	gatgttctca	tecactgace	gggccatgcg					
	241	catccgcctc	ctgcagcaga	tggagcagtt	catccagtac	cttgacgagc	caacagtcaa					
	301	cacccagatc	ttcccccacg	tcgtacatgg	cttcctggac	accaaccctg	ccatccggga					
			aagtccatgc									
			aagcactttg									
	481	caacaccaca	gtctgcctgg	gcaaaatcgg	ctcctacctc	agtgctagca	ccagacacag					
	541	ggtccttacc	tctgccttca	gccgagccac	tagggacccg	tttgcaccgt	cccgggttgc					
	601	gggtgtcctg	ggctttgctg-	ccacccacaa	cctctactca	atgaacgact	gtgcccagaa					
	661	gatcctgcct	gtgctctgcg	gtctcactgt	agatcctgag	aaatccgtgc	gagaccaggc					
			wttcggagct									
			gtggagaagg									
	841	agctagctgg	gcaggctggg	cgtgaccggg	gtctcctcac	tcacctccaa	gctgatccgt					
	901	tcgcacccaa	ccactgcccc	aacagaaacc	aacattcccc	aaagacccac	gcctgaagga					
			cagcccccac									
	1021	acgcaggagg	aggacaagga	cacagcagag	gacagcagca	ctgctgacag	atgggacgac					
			gcagcctgga									
			gccaagtgag									
			agtccgactg									
							cgagtataac					
	1321	tggggtggcc	cagagtccag	cgacaagggc	gaccccttcg	ctaccctgtc	tgcacgtccc					
							cgagactgac					
							gcgggagatg					
	1501	gaggccaaac	gcgccgagag	gaaggtgcca.	agggccccat	gaagctggga	gcccggaagc					
	1561	tggactgaac	cgtggcggtg	gcccttcccg	gctgcggaga	gcccgcccca	cagatgtatt					
							tacataatca					
			aaattctatt									
#/												

Figure 14C

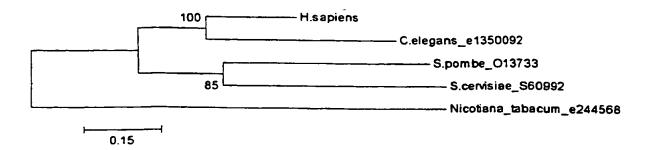


Figure 14B

Figure 14A

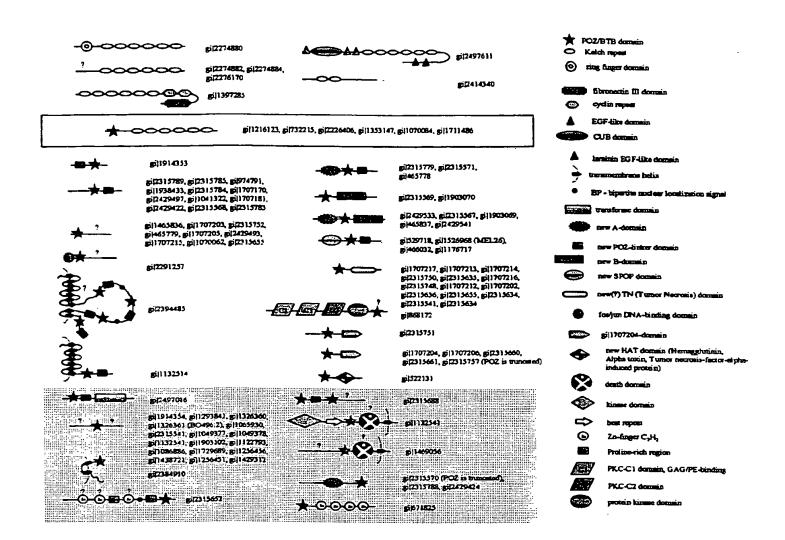


Figure 13

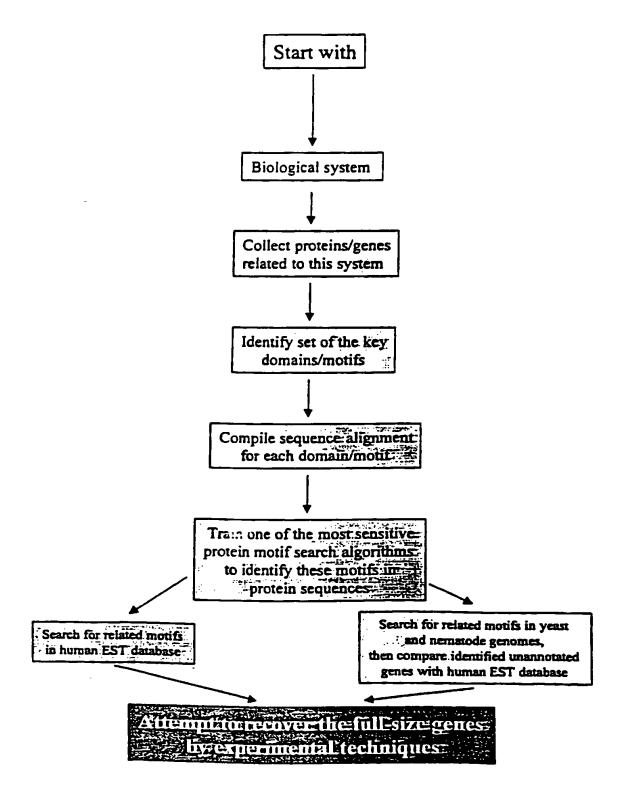
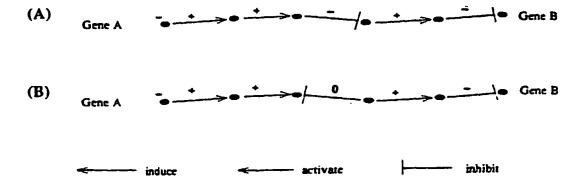


FIGURE 12



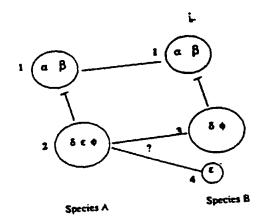


FIGURE 10

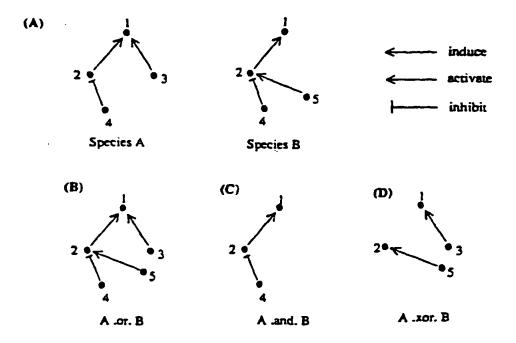


FIGURE 9

Start with Start with Start with a single Biological system a gene family a single gene Reconstruct a "network" of interacting genes and proteins Identify a set of key domains and motifs Search for related motifs in databases of known organisms Identify members of multigene families Compute phylogenetic trees Paralogous nevorks Identify clusters of paralogous genes, identify paralogous and orthologous fletworks Paralogous networks in human

Compare regulatory schemes, identify genes that are known in one but missing in another system.

Find the genes using experimental techniques.

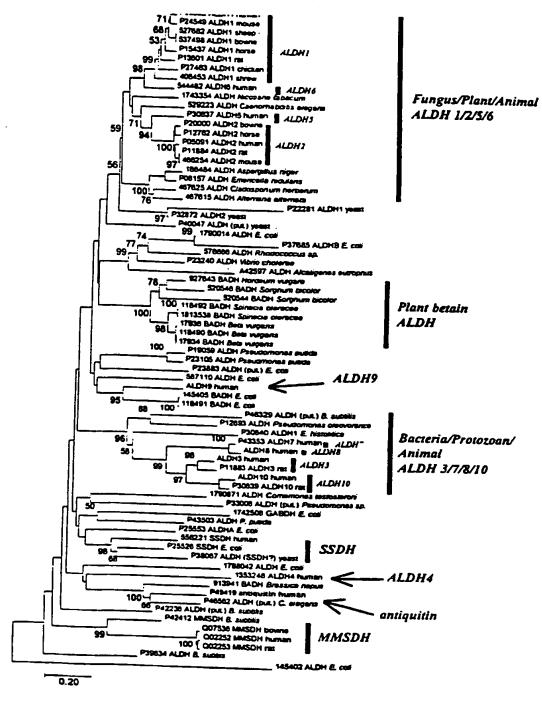
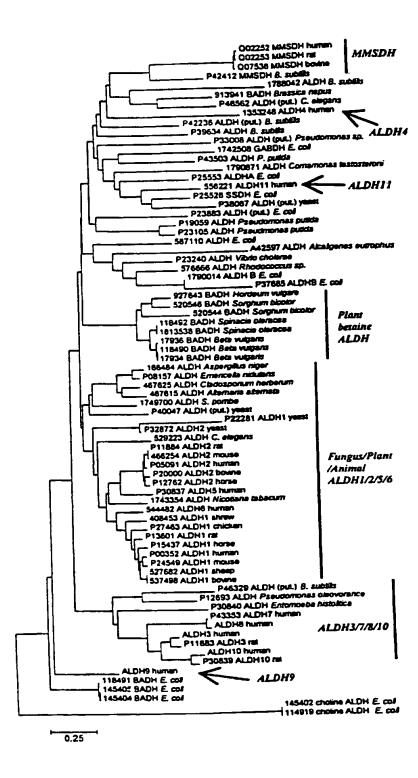


FIGURE ?



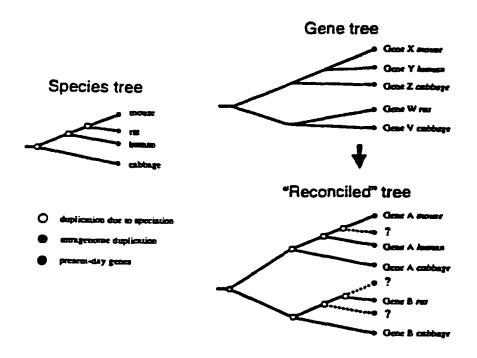
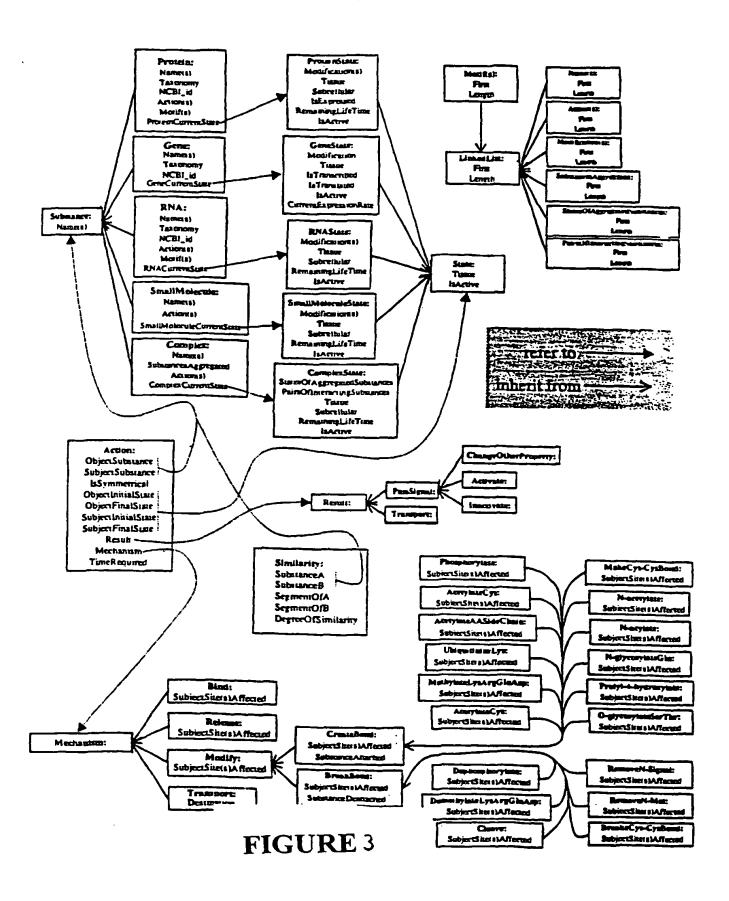


FIGURE 5

bcl-zl / bcl / bcl-zS / ccd-9 / Baz / Bik / Bak / p21 / NGFI-B / N10 / Nak1 / Nur7 / Nur7 | Nor-1 / Not-1 / RXR / galectin-1 / N-glycan / CNTF / Ick / fyn / ZAP-70 / raf / ras / MAP / protein kinase C / PEC / phosphatase calcineurin / NF-AT / AP1 / 14-3-3 / Raf-1 / Bcl-2 / Interteukin / IL-1 / IL-3 / cytokine / IGF-1 / CD95 / Apo-1 / RIP / FAF1 / FADD / FAP-1 / TNFR / TRAF / TRAP1 / TRAP2 / TRADD / HIAP1 / HIAP2 / CD40 / CD30 / XIAP / CD2 / CD3 / TCR / Bcl-w / Mcl-1 / NR-I3 / BHRF1 / HMWS-HL / E1B19K / Nbh / Mch2 / CPP32 / ICE / FLJCE / Nedd-2 / TX / Mch3 / Mch4 / ICB-1s / mx-1 / DNAse1 / caspase / MACB1 / Mch5 / apopain / Yamn / ICB / CMB / ccd-3 / ccd-4 / ccd-9 / p53 / MKE3 / MKE4 / MKE4 / MKE4 / BAG-1 / Src / FAST / p38 / p42 / ERK1 / p44 / ERK2 / SAPE / JNE / MEE / C-JUN / MEF2D / ATF2 / calcineurin / ELK-1 / protein phosphatase 2A / raf-1 / IL-1 brts / TNF / FTK / Apst / p35 / ETS / C-Myc / IL-2 / IL-2 receptor / NF-happs B / TNFR-1 / TRAIL / Apo-2L / DR4 / death receptor / DR3 / DR2 / DR5 / DR1 / bad / BMPR / BMP-2 / TGF / grim / bid / FAN / perforin / Fas-L / Fas / DcR1 / decoy receptor / wd-1 / NGF receptor / growth factor / RAR



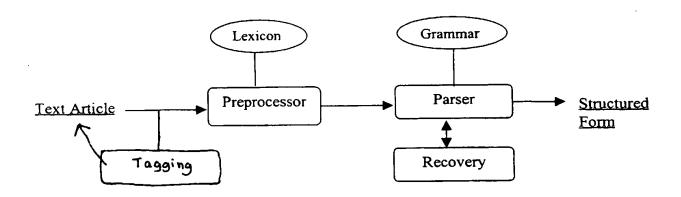


Figure 2

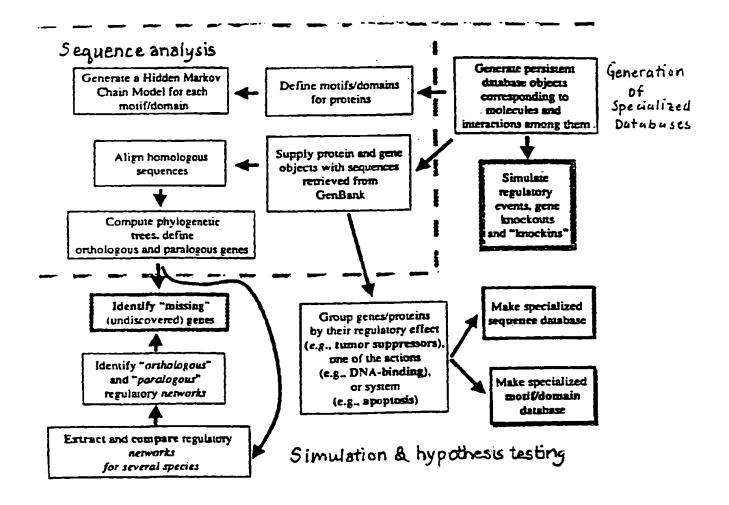


FIGURE 1

PCT/US00/10302

31. The system according to claim 22, wherein said error recovery means comprises:

means for segmenting the text data; and
means for analyzing the segmented text data to achieve at least a partial
parsing of the unsuccessfully parsed text data.

32. The system according to claim 22, wherein said tagging means comprises means for providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

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- 24. The system according to claim 22, further comprising means for referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.
- The system according to claim 22, wherein said parsing means
 further comprises means for segmenting the text data by sentences.
 - 26. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and means for segmenting each of the sentences at identified words or phrases.

27. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and means for segmenting each of the sentences at a prefix.

- 15 28. The system according to claim 22, wherein said parsing means further comprises means for skipping undefined words.
 - 29. The system according to claim 22, wherein said parsing means further comprises:

means for identifying one or more binary actions and their relationships;

20 and

means for identifying one or more arguments associated with the actions.

30. The system according to claim 22, further comprising means for performing error recovery when parsing of the text data is unsuccessful.

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- 17. The method according to claim 11, wherein said parsing step further comprises skipping undefined words.
- 18. The method according to claim 11, wherein said parsing step further comprises:

identifying one or more binary actions and their relationships; and identifying one or more arguments associated with the actions.

- 19. The method according to claim 11, further comprising performing error recovery when parsing of the text data is unsuccessful.
- The method according to claim 19, wherein said error recovery step comprises:

segmenting the text data; and analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

- 21. The method according to claim 11, wherein said tagging step

 comprises providing the structured data component in a Standard Generalized Markup

 Language (SGML) compatible format.
 - 22. A computer system for extracting information on biological entities from natural-language text data, comprising:
 - (i) means for parsing the natural-language text data; and
- 20 (ii) means for regularizing the parsed text data to form structured word terms.
- The system according to claim 22, further comprising means for preprocessing the data prior to parsing, with the preprocessing means comprising
 identifying biological entities.

10. The method of claim 9 further comprising using each identified expression sequence tag to search sequence databases for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA.

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- 11. A method for extracting information on interactions between biological entities from natural-language text data, comprising:
 - (i) parsing the text data to determine the grammatical structure of the text data ;and
 - (ii) regularizing the parsed text data to form structured word terms.
- 12. The method according to claim 11, further comprising preprocessing the data prior to parsing, with preprocessing comprising the step of identifying biological entities.
- 13. The method according to claim 11, further comprising referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.
 - 14. The method according to claim 11, wherein said parsing step further comprises segmenting the text data by sentences.
- The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and segmenting each of the sentences at identified words or phrases.

- 16. The method according to claim 11, wherein said parsing step further comprises:
- segmenting the text data by sentences; and segmenting each of the sentences at a prefix.

(v)	imputing the species tree and gene tree into an algorithm
	which integrates the species tree and the gene tree into a
	reconciled tree; and

(vi) identifying orthologous genes present in one species but missing in another.

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8. The method of claim 7 wherein the following algorithm is used to integrate the species tree and the gene tree into a reconciled tree:

(i) computing the similarity $\sigma(S_{gi}, S_{sj})$ for each pair of interior nodes from trees T_g and T_s ,

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- (ii) finding the maximum $\sigma(S_{qi},S_{si})$;
- (iii) saving S_{gi} as a new cluster of orthologs, save $\{S_{gi}\}$ $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution);
- (iv) eliminating S_{gi} from T_g ; T_g : = $T_g \setminus S_{gi}$;

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(v) repeating step (ii)-(iv) until T_g is non-empty.

9. A method for identifying a novel gene comprising the following steps:

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defining a motif or domain composition of a gene of interest;

 (ii) searching for sequences which correspond to nucleotide sequences in an expression sequence tag database or other cDNA databases using a program such as BLAST and retrieving the identified sequences;

- (iii) searching additional databases for expressed sequence tags containing the domains and motifs characteristic for the gene of interest with Hidden Markov Model of domains and motifs identified in step (i);
- (iv) identifying nucleotide sequences comprising the gene of interest.

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- 51 The method of claim 1 wherein the regulatory pathway is involved 4. in apoptosis. The method of claim 1 wherein the specific protein from the first 5. species is involved in tumor suppression. A method for identifying the affect of a gene knockout on a regulatory pathway comprising the following steps: identification of the shortest non-oriented pathway (i) connecting two gene products; assigning an initial sign value of "-" to the knockout since (ii) the knockout gene product is inactive; moving along the shortest pathway between the two gene (iii) products multiplying the sign with the sign of the next gene product in the pathway, wherein "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; and (iv) determining the final sign at the end of the pathway, wherein "-" indicates inhibition and "+" indicates induction or activation of the pathway. 7. a protein of interest comprising: (i) selecting a gene of interest and searching a database for
 - A method for identifying a novel nucleic acid molecule encoding
 - homologous sequences;
 - (ii) aligning the homologous sequences identified in step (i);
 - (iii) constructing a gene tree using the sequence alignment;
 - (iv) constructing a species tree;

CLAIMS

	1. A me	thod for identifying a novel nucleic acid molecule encoding	
a protein of interest comprising:			
	(i)	selecting a specific protein from a first species involved	
5		in a regulatory network of interest;	
	(ii)	identifying known proteins that act upstream and	
		downstream in the regulatory network of interest with	
		respect to the specific protein selected;	
	(iii)	constructing the regulatory network of interest from the	
10		proteins identified in step (ii);	
	(iv)	for each identified protein, select a domain or motif and	
		search by homology for related proteins in a second	
		species, wherein a related protein is defined as a protein	
		having a homologous domain or motif;	
15	(v)	producing a regulatory network for the second species,	
		wherein said regulatory network incorporates the	
		identified related proteins;	
	(vi)	comparing the regulatory network from the first species to	
		the regulatory network of said second species;	
20	(v)	identifying a protein present in a regulatory network for	
		one species but absent in the regulatory network of the	
		other species; and	
	(vi)	isolating a nucleic acid molecule encoding the protein	
		identified in step (v) in the species in which it is missing.	
25		nethod of Claim 1 wherein the nucleic acid molecule encodes	
	hun	nan protein.	

3. The method of claim 1 wherein the related proteins are orthologs.

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WI). The nucleotide sequence of the human *Mad3* gene is presented in Figure 17B. The deduced amino acid sequence of the gene is presented in Figure 17C. The translated sequence consists of 206 amino acid residues 81% of which are identical to mouse Mad3 protein. The alignment of human and mouse Mad3 proteins shown below was made using BLAST server at NCBI and is presented in Figure 17C.

Multiple alignment of the new sequence with sequences of known Mad proteins was made using Clustalw and viewed with the HitViewer. A gene tree was computed from this alignment using NJBOOT. Multiple alignment of the new sequence with sequences of known Mad proteins (Figure 17C) along with its position on gene tree (Figure 18B) shows that this new human gene found by the approach described above belongs to the family of Mad proteins and is the ortholog of mouse Mad3.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

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The gene tree shown in the Figure 20 was constructed in the following way. The protein sequences of known members of *Mad* gene family were extracted from GenBank database using NCBI Entrez keyword searches. The extracted sequences were aligned using multiple alignment program Clustalw running on Sun SPARC station. The quality of the multiple alignment was checked using program HitViewer Iterate (A. Rzhetsky, available upon request) and the redundant, non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences was realigned with Clustalw and a gene tree as presented in Figure 15A was computed from the alignment using program NJBOOT (http://genome6.cpmc.columbia.edu // andrey) running on Sun SPARC station and viewed with program TreeView (http://genome6.cpmc.columbia.edu // andrey).

The tree presented in Fig.19A clearly shows the relationships between three known mouse genes and their two human homologs. Attempts to find a missing human ortholog of the mouse *Mad3* gene in protein non-redundant database at NCBI using BLAST search did not identify any human homologs other than sequences that were already present on the tree, confirming the absence of a known human ortholog for Mad3 protein in the database.

In order to identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using Mad3 protein sequence as a query. Two EST were identified and are shown in Figure 17A.

Due to the nature of dbEST database this search produced only partial sequences of potential candidate genes. To obtain complete coding sequences (complete cds) of the genes, a search was conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST zs77e55.r1 (gb|AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj|C02407), thus indicating that the two EST sequences found during the initial TBLASTN search belong to the same gene.

The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqManII (DNASTAR Inc.,

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sites and apparently antagonize Myc-mediated activation of the same set of target genes.

During tissue development a shift from Myc:Max to MAD:Max complexes occurs coincidentally with the switch from cell proliferation to differentiation. The switch in heterocomplexes is thought to reflect a switch from activation to repression of common genes leading to cessation of proliferation, exiting the cell cycle and the beginning of cell differentiation. In differentiating neurons, primary keratinocytes, myeloid cell lines and probably other tissues the expression of different MAD:Max complexes appear in sequential order during the transition from cell proliferation to differentiation. The MAD3 expression appears first and it is restricted to proliferating cells prior to differentiation where it is co-expressed with two different member of Myc family, c-Myc or N-Myc. Mxi1 transcripts are detected in proliferating and differentiating cells whereas MAD1 and MAD4 were confined to post-mitotic cells. Because Myc expression is not always downregulated in post-mitotic cells, co-expression of Myc and MAD genes may result in competition for Max heterodimers thus providing promoting or inhibitory effect on cell proliferation.

The gene expression patterns, along with ability of Mad proteins to suppress *Myc*-dependent transformation, are consistent with a potential function of Mad genes as tumor suppressors. This view is supported by the fact that allelic loss and mutations were detected at the *Mxi1* locus in prostate cancers (Eagle et al., 1995 Nat Genet 9:249-55). Cloning of the murine proteins *Mad3* and *Mad4* as well as their relation to *Max* signaling network was described by Hurlin (Hurlin PJ, et al., 1995, EMBO J. 14:5646-59) and Queva (Queva et al. 1998 Oncogene 16:967-977). Human orthologs of *Mad4*, *Mad1* and *Mxi1* are known.

In this example, the discovery of an unknown human ortholog of *Mad3* protein found "in silico," by means of phylogenetic analysis of known mouse and human members of the *Mad* gene family and database searches is described. Since the function of murine *Mad3* as a *Max*-interacting transcriptional repressor of *Myc*-induced neoplastic transformation is well described, we can assign the same function to its human ortholog.

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protein (sp|P15533|RPT1) (Figure 13). Analysis of regulatory functions of RPT1 in the mouse reveals that this gene functions as a repressor of the interleukin 2 receptor (IL-2R) gene. When the RPT1 gene is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway in T lymphocytes resulting in an accumulation of T lymphocytes in blood. This result is consistent with aberrations observed in CLL, namely abnormal accumulation of B-cells in the blood (Trentin L. et al., 1997, Leuk. Lymphoma 27:35-42) and mutations in the human RPT1 gene play a role in development of CLL.

6.1.3 EXAMPLE: A DISCOVERY OF A HUMAN ORTHOLOG OF THE MURINE MAX-INTERACTING TRANSCRIPTIONAL REPRESSOR

The family of *Myc* proto-oncogenes encodes a set of transcription factors implicated in regulation of cell proliferation, differentiation, transformation and apoptosis. C-*Myc* null mutations result in retarded growth and development of mouse embryos and are lethal by 9-10 day of gestation. In contrast, overexpression of *Myc* genes inhibits cell differentiation and leads to neoplastic transformation.

Moreover, deregulation of *Myc* expression by retroviral transduction, chromosomal translocation or gene amplification is linked to a broad range of naturally occurring tumors in humans and other species.

Another protein, called Max, is an obligatory heterodimeric partner for Myc proteins in mediating their function as activators of transcription during cell cycle progression, neoplastic transformation and programmed cell death (apoptosis). In order to make an active transcription factor the Myc proteins must form heterodimers with Max protein. This interaction with Max protein is necessary for specific binding of Myc with CACGTG box (or related E-boxes) on DNA and for activation of promoters located proximal to the binding sites.

Besides the Myc family of transcription factors, the Max protein forms complexes with another family of so-called MAD proteins: Mxi1, MAD1, MAD3 and MAD4. Whereas Myc:Max complexes activate transcription, MAD:Max complexes work in an opposite way repressing the transcription through the same E-box binding

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The two closest human sequences, AA481214 and W51957, are depicted in Figure 14A. To determine whether the identified human sequences were orthologs or paralogs to the gi | 1132541 gene of *C. elegans*, a gene tree (Saito and Nei, 1997, Molecular Biol. Evol. 4:406-425) was computed. The gene tree was generated using homologous genes identified with a BLASTP search against NCBI non-redundant database, using the human EST AA481214 sequence as a query. The resulting tree indicates that the identified human EST AA481214 represents a true ortholog of the *C. elegans* gene gi | 1132541 (Figure 14B). The nucleotide sequence of the death domain protein is shown in Figure 14C, as well as the deduced amino acid sequence presented in Figure 14D.

6.1.2 APOPTOSIS GENE DISCOVERY METHOD

As a first step in identifying a novel gene involved in apoptosis, a comprehensive set of articles describing the system of apoptosis/programmed cell death in different species was compiled using the keyword "apoptosis". By analyzing the articles, information on regulatory pathways characterizing this system in different species, *i.e.*, *C. elegans*, mouse, fruit fly, chicken, and human, was extracted. The regulatory information was stored as a collection of schemes produced in PowerPoint (Microsoft). Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways. The keywords were used to generate a specialized sequence database, referred to as Apoptosis3, utilizing the PsiRetriever program for extraction of proteins from the all-inclusive non-redundant GenBank database (NCBI). Using program PsiRetriever, sequences from the non-redundant (NCBI) database of protein sequences, were retrieved and stored as a FASTA file. The FASTA file was then converted into binary blast database using program FORMATDB from the BLAST suit of programs.

Genomic and cDNA sequences located in the region of human chromosome 13q were compared with the Apoptosis3 database using BLASTALL program from BLAST program complex. This region of the human genome is associated with Chronic Lymphocytic Leukemia (CLL). The comparison revealed significant similarity between a CLL region open reading frame and the mouse RPT1

groupings of proteins: (i) proteins known to be tumor suppressors, and (ii) proteins implicated in apoptosis in animals were developed.

6.1 APOPTOSIS GENE DISCOVERY METHOD

Identification of a putative apoptosis-related human gene began with an identification of all genes in *C. elegans* that contained either a POZ or kelch domain. A subset of these genes is shown in Figure 13. Hidden Markov Models (HMM) for the POZ and Kelch domains were built as follows. Starting with POZ and kelch sequences from the *Drosophilia* kelch protein (gi | 577275) homologs were identified in other protein sequences using the BLASTP program. The resulting sequences showing significant similarity (e-value less than 0.001) were aligned using CLUSTALW program and the alignments were used to build Hidden Markov Models with HMMER-2 package (Krogh et al., 1995, :http://hmmer.wustl.edu/). A computer printout listing of HMM models of tumor suppressors appears as a Microfiche H to the present specification. (See, http://hmmer.wustl.edu; Chapter 2, which is incorporated by reference herein in its entirety, for a detailed description of HMM models)

The resulting models were used to search through a database collection of *C.elegans* protein sequences. The domain structures of proteins having either a POZ or kelch domain were identified using existing collections of protein domains (e.g., see http://blocks.fhcrc.org/blocks/blocks release.html, http://coot.embl-heidelberg.de/SMART/, http://www.motif.genome.ad.jp/). One of the unannotated protein-coding genes of *C. elegans* (corresponding protein accession number gi | 1132541, see Figure 11) appeared to include a POZ domain, death domain, kinase domain, and heat repeat. A death domain is characteristic for the apoptosis system and a kinase domain indicates that the protein is likely to participate in phosphorylation of other proteins. The presence of these particular domains suggests that this protein is serving as a regulatory protein.

Using the protein sequence of gi | 1132541, the database of human EST sequences was searched and a number of partial human cDNA sequences representing potential human orthologs or paralogs of the *C.elegans* gi | 1132541 were identified.

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In another embodiment, polymerase chain reaction (PCR) can be used to amplify the desired sequence from a genomic or cDNA library. To isolate orthologous or paralogous genes from other species, one synthesizes several different degenerate primers, for use in PCR reactions. In a preferred aspect, the oligonucleotide primers represent at least part of the gene comprising known ortholog or paralog sequences of different species. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the known nucleotide sequences and the nucleic acid homolog being isolated.

Synthetic oligonucleotides may be utilized as primers to amplify by PCR sequences from a source (RNA or DNA), preferably a cDNA library, of potential interest. PCR can be carried out, e.g., by use of a Perkin-Elmer Cetus thermal cycler and a thermostable polymerase, e.g., Amplitaq (Perkin-Elmer). The nucleic acids being amplified can include mRNA or cDNA or genomic DNA from any eukaryotic species. After successful amplification of a segment of a the gene of interest, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete cDNA or genomic clone.

Once identified and isolated the gene of interest can then be inserted into an appropriate cloning vector for amplification and/or expression in a host. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids and modified viruses, but the vector system must be compatible with the host cell used. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene). The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini.

6. EXAMPLE: USE OF SPECIALIZED DATABASES FOR IDENTIFICATION OF NOVEL GENES

To test the method of using databases for gene discovery, protein sequence and domain/motif databases specific to two overlapping functional

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carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10⁶ cpm ³²P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HC1 (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and reexposed to film. Other conditions of low stringency which may be used are well known in the art (e.g., as employed for cross species hybridizations).

In another specific embodiment, a nucleic acid which is hybridizable to a nucleic acid under conditions of moderate stringency is provided. For example, but not by way of limitation, procedures using such conditions of moderate stringency are as follows: filters containing DNA are pretreated for 6 h at 55°C in a solution containing 6X SSC, 5X Denhart's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution and 5-20 X 10⁶ CpM ³²P- labeled probe is used. Filters are incubated in the hybridization mixture for 18-20 h at 55°C, and then washed twice for 30 minutes at 60°C in a solution containing 1X SSC and 0.1% SDS. Filters are blotted dry and exposed for autoradiography. Other conditions of moderate stringency which may be used are well-known in the art. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.1% SDS.

For expression cloning (a technique commonly used in the art), an expression library is constructed. For example, mRNA is isolated from the cell type of interest, cDNA is made and ligated into an expression vector (e.g., a bacteriophage derivative) such that it is capable of being expressed by a host cell (e.g., a bacterium) into which it is then introduced. Various screening assays can then be used to select for the expressed gene product of interest based on the physical, chemical, or immunological properties of its expressed product. Such properties can be deduced from the properties of the corresponding orthologs from other species.

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knock out of gene A which can be any one of the following: inhibition of gene B, induction/activation of gene B, or none. In addition to the "electronic knock out", an "electronic knock in" of a particular gene can be simulated. In such a computer simulation, the artificial addition of a gene and its effect on a regulatory system may be analyzed.

5.6. IDENTIFICATION AND ISOLATION OF NOVEL GENES

The present invention relates to identification of novel genes, i.e., missing orthologs or paralogs, and the isolation of nucleic acid molecules encoding novel genes. In a specific embodiment, a nucleic acid molecule encoding a missing ortholog or paralog can be isolated using procedures well known to those skilled in the art (See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach MRL Press, Ltd., Oxford, U.K. Vol. I, II.).

For example, genomic and/or cDNA libraries may be screened with labeled DNA fragments derived from a known ortholog or paralog from a specific species and hybridized to the genomic or cDNA libraries generated from a different species. For cross species hybridization, low stringency conditions are preferred. For same species hybridization, moderately stringent conditions are preferred. Any eukaryotic cell potentially can serve as the nucleic acid source for the molecular cloning of the gene of interest. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell.

By way of example and not limitation, procedures using conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792; and Sambrook et al. 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring harbor, New York): Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HC1 (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 mg/ml denatured salmon sperm DNA. Hybridizations are

while the "object" substance can be in either active, or inactive, state depending on the action type. For example, the action "dephosphorylation" requires an active phosphatase ("subject" substance) and a phosphorylated substitute protein ("object" substance) in phosphorylated form. If both conditions are satisfied, the action is recorded as in progress. At termination, the substances must change their states as specified by the action. On each following "quantum" of time, the simulation proceeds in the same way while maintaining the "bookkeeping" of the remaining time for each action and the remaining lifespan of each substance. The simulation stops when there are no more active actions available. The program allows editing of the properties of the objects, changing the scale and focus of the visualized simulation, and experimenting with the systems output.

In a specific embodiment of the invention a "knock out" of a gene can be simulated to model the regulatory system that normally includes hypothetical gene A. One of the typical questions related to the gene knock out is how does the knock out affect a biological pathway of interest. A hypothetical example of evaluating the impact of a knock out of hypothetical gene A on the expression of a hypothetical gene B is shown in Figure 12. The answer to such a question could be "gene B will be inhibited" or "gene B will be induced" or "no effect".

In the practice of the present invention, a simple algorithm involving multiplication of gene interaction "signs" along the shortest pathway between the genes can be used to determine the outcome. The algorithm involves the following steps: (i) identification of the shortest non-oriented pathway connecting genes A and B involved in a pathway of interest; (ii) assigning sign "-" to gene A since it is knocked out and taking this sign as the initial sign value; (iii) moving along the shortest pathway between genes A and B, multiplying the current value of the sign with the sign of the next arc, where "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; (iv) determining if the final result of multiplication is "0", if so eliminating the zero arc and trying to find the shortest oriented bypass pathway between A and B in the remaining network; otherwise stop. The final value of the sign at the moment of arriving at vertex B would indicate the most likely effect of the

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The present invention encompasses the nucleic acid molecule of Figure 14C, comprising the sequence of EST AA481214 and proteins encoded by said nucleic acid molecule. The invention also relates to nucleic acid molecules capable of hybridizing to such a nucleic acid molecule under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

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5.5.3. SIMULATION OF REGULATORY CASCADES

In an embodiment of the invention, an interactive graphical program is utilized for visualizing the scheme of regulatory relationships, "current" states of the substances, and active and inactive actions between pairs of substances. Such a program can be utilized for identification of genes which are associated with a specific disease. Currently, disease associated genes are discovered through positional cloning methods which combine methods of genetics and physical mapping with mutational analysis. The present invention provides a novel method for discovering disease associated genes. For simulating regulatory cascades, it is assumed that the time in a simulated regulatory system advances in discrete "quanta," or periods of time. The "state of substances" of the system for each discrete period of time is computed by: creating a set of substance objects, where a set of interactions between each created substance object is known, an initial state is specified. The time is initially set to zero. All defined actions are observed to confirm that the substances corresponding to the actions (i) exist, and (ii) are in the right initial states. Action is defined by a pair of substances that are in suitable states. The "subject" substance is in the inactive state,

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including for example yeast and/or nematode genes, that bear a significant similarity to the gene of interest or a specified domain of the corresponding protein are collected. Third, the identified genes are in turn subjected to a "domain analysis" to establish protein motifs which might suggest a function of these genes using, for example, HMMER software. Fourth, the selected genes are in turn used for database searches in EST databases (dbEST) and/or a non-redundant (nr) database to identify unknown genes that are potentially orthologous to the selected yeast and nematode genes. Once identified ESTs having different tumor suppressor domains may be linked using multiple PCR primers. Using routine cloning techniques, well known to those of skill in the art, a full length cDNA representing the gene of interest can be obtained.

Once new genes are identified by domain/motif analysis experimental searches may be carried out to isolate complete coding sequences and evaluate their tissue- and disease-specific expression patterns. In parallel their position with respect to regulatory networks can be identified as described below.

In a specific embodiment of the invention, an apoptosis related human gene was identified using the method described above. As a first step *C. elegans* genes containing either POZ or Kelch domains were identified. A Hidden Markov Model was developed using POZ and Kelch sequences from the *Drosophila* Kelch protein and any identified homologs. The resulting Hidden Marker Model was used to search through the collection of *C. elegans* protein sequences. One of the identified *C. elegans* genes contained a POZ domain, death domain, kinase domain and heat repeat. The presence of both a death domain and a kinase domain suggested that the protein functions as a regulatory protein.

A human EST database was searched using the protein sequence of the identified *C. elegans* gene and two sequences were identified (Figure 14A). A gene tree was computed to determine whether the identified human sequences were orthologs of the *C. elegans* gene. As depicted in Figure 14B, the human EST AA481214 appears to be a true ortholog of the *C. elegans* gene. Figure 14C presents the nucleotide sequence of the identified death domain gene. Figure 14D presents the amino acid sequence of the death domain protein.

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orthologous proteins with pairs of orthologous domains. After this correction, homologous networks are compared as described above.

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (lane 2) for species A and three hypothetical proteins (lanes 1, 3, and 4) for species B. Protein 1 in both species has motifs α and β , protein 2 has motifs δ , ϵ , and ζ , and proteins 3 and 4 have motifs δ and ζ , and ϵ , respectively. The motif analysis indicates that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A.

5.5.2 GENE DISCOVERY BASED ON PROTEIN MOTIF/DOMAIN SEARCHES

The present invention provides yet another method for identifying genes that are homologous and perform the same or an analogous function in different species. The method of the invention comprises the following steps: (i) creating a database of sequences which comprise a motif or domain composition of a gene of interest using, for example, HMMER software; and (ii) searching additional databases for expressed sequence tags (ESTs) containing the domains and motifs characteristic for the gene of interest with HMMs of domains and motifs identified in step (i). In yet another embodiment of the invention, sequences may be searched which correspond to nucleotide sequences in an EST database or other cDNA databases using a program such as BLAST and retrieving the identified sequences. In an optional step, for each EST identified, sequence databases can be searched for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA. Once identified, the ESTs can be used to isolate full length nucleotide sequences comprising the gene of interest using methods such as those described in Section 5.4, infra.

The general flowchart scheme for gene discovery analysis based on motif/domain search is shown in Figure 11. In a specific embodiment of the invention, the method referred to as the "phylogenetic reflection technique" comprises, first, defining the motif or domain composition of a gene of interest involved in a biological system of interest. Second, protein-coding genes from other species,

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In a specific embodiment of the invention a set of regulatory networks from different species, relating to the same biological system, apoptosis, for example, can be analyzed and visualized utilizing the following methods: (i) for each species functional information is collected relating to apoptosis; (ii) using the functional information, regulatory networks for each species comprised of interacting proteins and/or the genes involved in apoptosis are generated; (iii) the sequences of the interacting proteins and genes of each of the regulatory network are compared and for sequences showing similarity above a predetermined threshold range; and (iv) distinguishing between orthologs and paralogs using the methods set forth above.

An analysis similar to that performed using subtrees of sequences may be applied to classify protein functions as orthologous or paralogous actions. A "generalized" regulatory network maybe represented as a network wherein a substance as it occurs in a particular species is substituted with a cluster (i.e., subtree) of orthologous substances among species. In the final step of the analysis the clusters within each species are compared to one another, to identify missing genes.

Figure 11 depicts the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. As indicated in Figure 11A, an overlay of regulatory data for two species overlaps, but not completely. As indicated, protein 5 is known only for species B while protein 3 is known only for species A. The proteins in different species denoted with the same numeral are considered orthologous. As indicated, the regulatory relationships between a pair of proteins can be of three different kinds. Figure 9B, 9C, and 9D represent Boolean operations, OR, AND, and XOR, as arcs of the two regulatory relationships depicted in Figure 9A, the same operations being applicable to the set of vertices of the two regulatory relationships.

In some instances, orthologous networks in two distantly related taxa may have the same domains but arrangement of the domains between the related taxa may be different. In such a case, a one-to-one correspondence between orthologous proteins in closely related species has to be substituted with a one-to-many relationship among domains comprised within the proteins. For this purpose, a similarity object may be defined operating on pairs of motifs/domains in two proteins, and substitute pairs of

other species. The identified sequences are compared and for each pair of sequences showing similarity above a certain threshold, a similarity object is generated. A similarity object is generated if two sequences, nucleotide or amino acid, show significant similarity in database searches (p value < 0.001). The object retains the following information: (i) reference to similar substances *i.e.*, genes or proteins; (ii) significance of the similarity, similarity score and percent of identity; and (iii) coordinates of the similarity region within two compared sequences.

"Orthology objects" constitute a subset of "similarity objects" which satisfies one additional requirement, *i.e.*, that two similar sequences should be identified as orthologs by the tree-based algorithm described above. In identifying orthologs, if gene A is orthologous to gene B, and gene B is orthologous to gene C, gene A is necessarily orthologous to gene C.

In a specific embodiment of the invention, for each species under analysis, orthologous proteins or genes are identified. In a further embodiment of the invention, small orthologous molecules participating in a regulatory network for two or more species may also be identified. Where proteins, genes, or molecules are orthologs, the action of the protein, gene or molecule between species may be interchangeable. If more than two species are involved in the analysis, subtrees of orthologous substances and subtrees of orthologous actions are identified.

Once orthologous genes, proteins or molecules are identified in two or more species, by forming a reconciled tree, for example, a set of orthologous or paralogous regulatory networks can be analyzed and visualized using graph theory where arcs represent actions and vertices represent substances. Thus, the method of the invention may further comprise the following steps: (i) superimposing the orthologous regulatory networks from two or more species and searching for the actions (arcs) and substances (vertices) in the homologous networks that are represented in some taxa but absent in others; (ii) superimposing paralogous regulatory networks from the same taxa and searching for paralogous genes that are missing in some taxa; and (iii) computing a general regulatory network that summarizes common regulatory sequence relationships known for more than one species.

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multigene families through comparisons of regulatory networks for different species, searching expressed sequence tag (EST) databases, and simulation of regulatory cascades.

5.5.1. GENE DISCOVERY THROUGH ANALYSIS OF REGULATORY NETWORKS

The present invention provides a method for identifying undiscovered genes through comparisons of regulatory networks for different species where functionally similar regulatory systems are conserved. The amount of information available concerning regulatory genes and/or proteins in different organisms and their functional relationships allows one to reconstruct and compare regulatory networks. Since in most cases, the knowledge of all genes involved in almost any particular regulatory system is incomplete, a comparison of homologous networks within the same organism and between different species permits the identification of genes absent in a system under comparison.

The identified genes, being part of a regulatory network, are implicated as potentially contributing to a phenotype of a disease associated with the system under analysis. Using the methods of the present invention these putative disease genes can be cloned, mapped and analyzed for mutations directly, thereby omitting the expensive and time-consuming steps of positional cloning and sequencing of genomic regions. Gene discovery by analysis of regulatory networks is outlined in Figure 8. The analysis is initiated starting with a biological system (e.g., signaling pathway of genes involved in Bcl-2-regulated apoptosis in lymphocytes), a single gene (e.g., Bcl-2) or a gene family (e.g., caspases).

Initially, a specialized database is generated for comparison of regulatory networks between different species. For example, starting with a single candidate gene in a single species, a typical iteration in this process begins with identification of all known proteins and genes that are upstream and downstream with respect to it in regulatory hierarchies and the reconstruction of a network of interacting genes and proteins. Next, for each protein, a set of key domains and motifs is identified and this information is used to search for related proteins in humans and

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conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST Zs77e55.rl (gb/AA278224) as the search query. The search identified a single overlapping sequence. The search for overlapping sequences was performed using program Iterate with EST zs77e55.rl (gb/AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj/C02407), thus showing that the two EST sequences found during the initial TBLASTIN search belong to the same gene. The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqMan11(DNASTAR Inc., WI). The nucleotide sequence of the human Mad3 gene is presented in Figure 17B. The deduced amino acid sequence of which is presented in Figure 17C. The complete DNA sequence is also shown.

The present invention relates to nucleic acid molecules encoding the human Mad3 protein shown in Figure 17C. The invention also relates to nucleic acid molecules that hybridize to the nucleic acid molecule of Figure 17B under conditions of high stringency and encode a Mad3 protein. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of 32P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5. SIMULATION AND HYPOTHESIS TESTING

The simulation and hypothesis testing methods of the invention, described in the subsections below, utilize specialized databases of gene/protein structures and interactions for identifying potentially undiscovered members of

Then define similarity measure, σ , between S_{gi} and S_{sj} in the following way:

$$\sigma(S_{gi},S_{sj}) = 0 \text{ if } |S_{gi}| \neq |\{S_{gi}\}|, \text{ or } S_{sj}(S_{gi}) \neq S_{gi}, \text{ and}$$

$$\sigma(S_{gi},S_{gi}) = |S_{gi}|$$

The support of tree clusters by data can be measured using the bootstrap technique described in Felsenstein (1985, Evolution 39:783-791).

In an embodiment of the invention, the human antiquitin gene was identified using phylogenetic analysis. The aldehyde dehydrogenase gene family in humans can be subdivided into at least ten ancient subtrees characterized by different functions of corresponding proteins. These genes probably arose from a series of gene duplications of an ancestral gene which took place before the divergence of a common ancestor of Eukaryotes and Eubacteria.

The aldehyde dehydrogenase gene cluster is highlighted in Figure 6 which shows the original tree of ALDH sequences, the circled area indicating a sequence cluster where bacterial (*Bacillus subtilis*), plant (*Brassica napus*), and nematode (*Caenorhabditis elegans*) ortholog is present, but a human ortholog is not known. A random screening of cDNA libraries showed that a human ortholog, referred to as antiquitin, does exist. Figure 7 shows the same gene tree as in Figure 6 with an additional human protein referred to as antiquitin present in the tree.

In yet another embodiment of the invention, a human ortholog of the murine Max-interacting transcriptional repressor Mad3 was identified through phylogenetic analysis of a gene family. The gene tree was constructed as follows. The protein sequences of known members of the *Mad* gene family were extracted from GenBank database. The extracted sequences were aligned using multiple alignment program CLUSTALW running on Sun SPARC station. Redundant and non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences were realigned with CLUSTALW and a gene tree as presented in Figure 18A was computed. To identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using mouse Mad3 protein sequences as a query. Two highly homologous ESTs were identified and are presented in Figure 17A. To obtain a complete coding sequence a search was

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subtrees of orthologs in a gene tree, and then comparing the subtree in the gene tree with a species tree. A missing gene appears as a branch present in the species tree but absent in the gene tree. The algorithm for defining an orthologous gene subtree and predicting the undiscovered, or lost in evolution, genes is as follows:

Let T_g be the most likely gene tree identified with one of consistent tree-making methods from a set of properly aligned homologous genes $\{1, 2, ..., s\}$, such that one or more homologous genes from every species corresponds to pending vertices of T_g . Each gene is labeled with the species it comes from (1,...,s) adding subscripts to distinguish homologous genes from the same species whenever it is necessary. Let T_g be the true species tree (tree correctly reflecting speciation events which we assume to be known) for species $\{1, 2, ..., s\}$. Due to the biological meaning of T_s each species in this tree is represented only once. It is assumed that both T_s and T_g are binary, although it is straightforward to extend the algorithm described here to the case of multifurcated trees.

15 Algorithm

- A1. For each pair of interior nodes from trees T_g and T_s , compute similarity $\sigma(S_{gi},S_{si})$.
- A2. Find the maximum $\sigma(S_{gi}, S_{si})$.
- A3. Save S_{gi} as a new subtree of orthologs, save $\{S_{gi}\}$ $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution).
- A4. Eliminate S_{gi} from T_g ; $T_g := T_g \setminus S_{gi}$.
- A5. Continue A2 A4 until T_g is non-empty.

The following definitions apply:

Let Sgi be an ith subtree of Tg (corresponding to the ith interior node),

correspondingly, let S_{sj} be jth subtree of tree T_s .

Let $\{S_{gi}\}$ stand for an unordered set of species represented in S_{gi} such that each species is represented exactly once, and let $|\{S_{gi}\}|$ and $\{|S_{gi}|\}$ be the number of entries in $\{S_{gi}\}$ and the number of pending vertices in S_{gi} , respectively. Define by $S_{sj}(S_{gi})$ the unique subtree of S_{sj} that has leaves labeled exclusively with species from $|\{S_{gi}\}|$, so that each element of $|\{S_{gi}\}|$ is used i.e., that is, the unique subtree

obtained by eliminating from S_{sj} all species that are not present in $|\{S_{gi}\}|$.

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By applying phylogenetic analysis, *i.e.*, reconstruction of gene trees of gene/protein sequences, one can predict the existence of undiscovered genes in humans and other species in addition to identifying the function of a gene. Such a technique is a significantly more powerful tool for identification of new genes than mere sequence comparisons.

Methods of computing gene trees from a set of aligned sequences include the: (i) heuristic method based on an optimization principle which is not directly motivated by a probability model (Fitch, 1974 J. Mol. Evol. 3:263-268)), (ii) the maximum likelihood method (Goldman, 1990, Syst. Zool. 30:345-361; Yang et al., 1995, Syst. Biol. 44:384-399; Felsenstein, J., 1996, Methods Enzymol. 266-418-427); and (iii) the distance matrix tree making method (Saito, N. and Nei, M., 1987, Mol. Biol. Evol. 4:406-425). Since the data analyses of orthologs and paralogs often involve very distantly related sequences, the maximum likelihood method is preferably used for small data sets and the distance-matrix method in other instances.

To construct a reconciled tree according to the invention, the first step comprises a search for homologs in a publicly or privately available database such as, for example, GenBank, Incyte, binary BLAST databases, Swiss Prot and NCBI databases. Following the identification of homologous sequences a global alignment is performed using, for example, the CLUSTALW program. From the sequence alignment a gene tree is constructed using, for example, the computer program CLUSTLAW which utilizes the neighbor-joining method of Saito and Nei (1997, Mol. Biol. Evol. 4:406-425). Construction of a species tree is then retrieved from, for example, the following web site:

http://www.3.NCBI.NLM.NIH.GOV//taxomy.tax.html.

The species tree and gene tree are given as input into the algorithm described below, which integrates both trees into a reconciled tree. Agreement between the gene tree and the corresponding species tree for any given set of sequences indicates the identification of orthologs. In contrast, disagreement between the species and gene tree suggest a gene duplication that resulted in the formation of a paralog. Thus, through generation of a reconciled tree one can identify orthologs present in one species but missing in another. These can be deduced by forming

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amino acid or nucleotide replacements per site or in terms of millions of years (absolute geological time). In the former case, the average replacement rate in the majority of the published trees varies among tree branches, and the root-to-tip distances are different for different present day sequences. In the latter case, all root-to-tip distances are equal and the height of each interior node of the tree corresponds to the absolute geological time passed since the gene duplication corresponding to the interior node took place.

If a gene is unique, *i.e.*, represented with a single copy per genome rather than being a member of a family of similar genes, the correct gene tree depicting the origin of this gene in a few different species is identical to the species tree. In many instances, a single ancestral gene has been duplicated repeatedly during evolution to form a multigene family. A gene tree is constructed from a gene as it occurs in several species and reflects both speciation events and gene duplications within the same genome. Two homologous genes taken from different species that originated from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originated from the common ancestor via a series of events involving intragenomic duplications, or conversions, are called paralogs. The terms "ortholog" and "paralog" are applied to both nucleic acid and proteins herein.

If gene deletions are forbidden and all genes for all species represented in the tree are known, the gene tree can be reconfigured to recapitulate the species tree, such that each subtree contains only orthologous genes. This tree is referred to as a reconciled tree and is shown in Figure 5. Imperfect gene trees which contain incorrect or partial species subtrees can be used to build reconciled trees that indicate events of speciation, gene loss, and gene duplication.

Orthologs from different species in gene trees are usually clustered together, so that if all the existing homologous genes from different species were known, the same relationship of species would be recapitulated in each cluster of orthologous genes. Since in reality a considerable number of genes are not yet identified, the real gene trees contain incomplete clusters of orthologs that can be used for identification of the missing genes.

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lymphocyte apoptosis. This result indicates that the identified human Rpt1 homology may represent the gene in which genetic defects lead to CLL.

The amino acid sequence of the human Rpt1 gene is presented in Figure 15. The present invention relates to nucleic acid molecules encoding the human Rpt1 protein shown in Figure 15. The invention also relates to nucleic acid molecules capable of hybridizing to a nucleic acid molecule encoding the human Rpt1 protein presented in Figure 15 under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50 mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of ³²P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1 x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.4. GENE DISCOVERY THROUGH PHYLOGENETIC ANALYSIS OF GENE FAMILIES

The present invention provides a method for identifying novel genes comprising the following steps: (i) comparing a single sequence with a database; (ii) processing the output into a sequence alignment; (iii) computing gene trees; and (iv) analyzing the trees to predict the existence of undiscovered genes.

Figure 5 shows a "species tree," a "gene tree" and a "reconciled tree".

A "species tree", as defined herein, is a graph depicting the correct order of speciation events leading to a set of present day species as defined by taxonomy. A "gene tree" is a graphical representation of the evolution of a gene from a single ancestral sequence in a common progenitor to a set of present-day sequences in different species. Where gene duplication has occurred, a branch is bifurcated. The branch lengths of a gene tree are most frequently measured either in terms of the number of

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Once developed, the specialized databases can be used to identify novel genes based on computation and analysis of phylogenetic trees for multigene families and analysis of homologous regulatory networks.

In a specific embodiment of the invention, a specialized database was generated using a set of keywords defining proteins involved in apoptosis (see, Figure 4). The specialized sequence database was referred to as Apoptosis 3. As a first step in generating the specialized database, a comprehensive set of articles describing the system of apoptosis or programed cell death was compiled. The articles were analyzed and information on regulatory pathways characterizing apoptosis from a variety of different organisms was extracted. Such pathways included those involved in MHC-T cell receptor interactions, inflammatory cytokine signal transduction, induction by light, γ-radiation, hyperosmolarity or heat shock, pathways involving immunoregulatory receptors or receptors having cytoplasmic domains, integrin-related pathways and perforin/granzymeβ related pathways. The collected information was stored using Powerpoint (Microsoft) as a collection of graph/plots depicting the regulatory pathway. In addition, a list of proteins relevant to regulation of apoptosis was compiled.

Using the program Psi Retriever, sequences encoding the proteins relevant to regulation of apoptosis were retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file was then converted to a binary blast database using the program FORMATDB from the BLAST suit of programs. The BLAST suit of programs provides a set of programs for very fast comparisons of a single sequence to a large database. Both the database and the search or query sequence can be any combination of nucleotide and/or amino acid sequences.

In a working example described herein, the Apoptosis 3 database was used to compare genomic and cDNA sequences derived from the 13q region of human chromosome 13. This region of the chromosome is associated with Chronic Lymphocytic Leukemia (CLL). Using this method of analysis a human gene with significant homology to the mouse Rpt1 gene was identified. When the activity of Rpt1 is knocked out in mice, the regulatory effect is manifested as a block in T-

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interactions between them. Such databases are particularly useful for computation and analysis of regulatory networks between proteins. The semantic model is designed for representing substances, such as proteins and actions between them, and is based on widely accepted principles of object-oriented programming languages such as Java. Figure 3 is a diagram illustrating the object representation of molecules and relations between them. As indicated in Figure 3 there are six major classes, corresponding to the top-level classification of objects and actions: (i) a substance; (ii) a state of a substance; (iii) a similarity between substances; (iv) an action between substances; (v) a result of the action; and (vi) a mechanism that enables an action.

Figure 3 presents the class design graphically, listing the variables that represent the properties of each class or class object in the implementation. Classes can be made nested via the mechanism of "inheritance", i.e., classes are defined starting with the most general ones and moving towards more specific classes.

Definition of more specific classes is simplified because the properties of the general classes are "inherited" by the specific classes and need not be redefined each time (see, Flanagan 1997, Java in a Nutshell, Second Edition. O'Reilley & Associates, Inc. Sebastopol, CA).

As shown in Figure 3, the two key object types in this scheme are substances (nodes of the graph representing regulatory networks) and actions (oriented edges connecting pairs of nodes), while result and mechanism objects are auxiliary to object action. Each substance object is characterized with a state. In this scheme, action is the most complicated object; each action object is characterized by a specific pair of substances participating in the action, one of which can be active and is referred to as Subject Substance and the second of which can serve as a substrate for the former and is referred to as Object Substance. Furthermore, for each action the initial and final states corresponding to interacting substances are defined. The property Time Required of each Action Object allows the setting of different durations for different actions (time is measured in relative units; see René Thomas and Richard D'Ari, 1990, "Biological Feedback," CRC Press Boca Raton, Ann Arbor, Boston).

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Hidden Markov Model method for building domain/motif models include neural network motif analysis (Wu, C.H. et al., 1996, Comput Appl Biosci 12, 109-18; Hirst, J.D., 1991, Protein Eng 4:615-23) and positional weight matrix analysis (Claverie, J.M., 1994, Comput Chem 18:287-94; Venezia, D., 1993, Comput Appl Biosci 9:65-9; Bucher, P. 1996, Comput Chem, 20:3-23; Tatusov, R.L., 1994, Proc Natl Acad Sci USA 91:12091-5).

Once a comprehensive collection of motifs/domains is created, each particular protein may be compared against a complete database of HMMs to identify known motifs and domains.

- 10 The Hidden Markov Model (HMM) is built using the following steps:
 - A1. Start with a motif/domain name and a single amino acid sequence representing a domain or motif.
 - A2. Do PSI-BLAST (BLASTPGP) search with the motif/domain sequence against a protein non-redundant database.
 - A3. Retrieve the sequences identified in the database search from the protein sequence database. Exclude low-complexity sequences, short or incomplete sequences and sequences with similarity score above a selected threshold of PPD value <0.001
 - A4. Align the set of sequences with CLUSTALW (or other multiple sequence alignment program).
 - A5. Use the set of aligned sequences for building HMM with the programs provided with HMMER and HMMER2 packages (see Hughey and Krogh 1996, J. Mol. Biol. 235:1501-1531).
 - A6. Do a new database search comparing new HMM with the non-redundant protein database.
 - A7. Continue steps A3-A6 until the convergence of the Markov model *i.e.*, until no new sequences are identified, or the maximum allowed number of iterations as defined by the user is reached. (Hugh R. and Krogh A., 1996, Comput. Appl. Biosci. 12: 95-107).
- In addition, in yet another embodiment of the invention, a specialized database may be designed to contain a semantic model of proteins and of the possible

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For example, but not by way of limitation, a specialized database may be prepared as follows. Protein and gene sequences may be provided, for example, by the Java program PsiRetrieve which allows for quick retrieval of protein or nucleotide sequences from binary BLAST databases by sequence accession number, keyword or groups of keywords, or species name. In addition, using the program PsiRetriever, sequences encoding the proteins of interest may be retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file is then converted into a binary blast database using the program FORMATDB from the BLAST suit of programs.

Known motifs/domains for proteins may also be collected using the flat file versions of major protein databases, such as SwissProt (http://expasy.hcage.ch/sprot) and the non-redundant database of NCBI (http://www3.ncbi.nlm.nih.gov). The databases can be downloaded and searched for the keywords "motif" and "domain" in the feature tables of proteins. In addition, existing databases of motifs and domains, such as BLOCKS (http://dupsas.Weizmann.ac.il/bcd/bcdparent//databanksblocks/hfml) and pfam(http://www.sanger.ac.uk//software/pfam; http://pfm.wustl.edu), can be downloaded (Henikoff et al., 1991, NAR 19:6565-6572). Still further, it is understood that any publically available database containing gene/protein sequences may be 20 utilized to generate the specialized databases for use in the practice of the present invention.

Homologous sequences may be aligned using, for example, the CLUSTALW program (Higgins, et al. 1996 Methods in Enzymology 266: 383-402). A protein's sequence corresponding to each domain/motif can be identified, saved and used for building a Hidden Markov Model (HMM) of the domain/motif using a HMMER and HMMER2 packages (see, Durbin, R. et al. 1998 in Biological Sequence Analysis: Probablistic Models of Proteins and Nucleic Acids). HMMER and HMMER2 packages are useful for (i) building HMMs from sets of aligned protein or nucleotide sequences, and (ii) comparing the HMMs with sequence databases aimed at identifying significant similarities of HMMs with database sequences. Both nucleotide and protein databases can be used for this purpose. Alternatives to the

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Working with nucleotides implies that errors involving reading frames must be addressed. For example, working with a code of four letters, the nucleotide combination ATCTGTCACG could mean ATCT/GTCA or TCTG/TCAC or CTGT/CACG. Since the text is translated into a nucleotide combination, only one of these possibilities is correct. But BLAST can not distinguish between these solutions, i.e., BLAST would potentially match a database sequence to a wrong reading frame in the query sequence, producing many nonsense results that could compromise the significance of true results.

The solution to this problem is a comma-free code. A comma free code knows only one correct reading frame. BLAST therefore does not produce any nonsense results. A comma-free code consists of only one permutation of a nucleotide combination. For example, given the nucleotide combination ATCC and its permutations CATC, CCAT and TCCA, only ONE of these permutations would be included in a comma-free code. The code in Appendix E does represent a comma free code. Comma-free codes were discussed in the early days of DNA research (Crick et al., Proc. Natl. Acad. Sci. 43:416-421).

In order to fine-tune the matching process, different BLAST parameters must be adjusted, for example: word size (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs);mismatch penalty (exact vs approximate matching); numbers of alignments to show (true matches of low significance can sometimes be at the very end of the BLAST output, therefore many alignments have to be shown); and expectation value (which sets the significance value for matches in the output file).

5.3. GENERATION OF SPECIALIZED DATABASES

In accordance with the present invention, specialized databases may be developed that contain information derived from unpublished data, publications such as research articles, theses, posters, abstracts, etc. and/or databases concerning interactions among genes and proteins, their domain/motif structure, and their biological functions.

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In addition, the script looks for plurals of words. For example, "interleukins" should be recognized as a protein name, although only the singular form, "interleukin", is in the database.

The final result consists of the original journal article with XML tags surrounding the gene and protein names. This is done using the same script as in Appendix G:

blocked <phr sem="gp">T cell antigen receptor</phr> (TCR)- and <phr sem="gp">CD28</phr>-mediated <phr sem="gp">IL-2</phr> gene transcription. Therefore, <phr sem="gp">Rap1</phr> functions as a negative regulator of...

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names.

BLAST is sensitive to the search space the program works in. Thus, given a long query sequence and a large sequence database, matches have a lower statistical significance because the chances are higher that the matches could have occurred by chance alone. In addition, matches with few letters have a lower statistical significance than matches with many letters. In order to find all true matches with any significance level, some measures were undertaken to address this problem. For example, (i) the query sequence was divided into 10 equal length parts, i.e., the journal article was divided into 10 parts and 10 different queries are run on each part separately; (ii) the sequence database (with the gene and protein names) is separated into 5 databases, each containing protein/gene names of different length; (iii) gene and protein names with less than 3 letters in the database were 'expanded', i.e., spaces were added at the beginning and the end of the name. Doing so, the statistical significance of a match containing a short name was higher. A space does not only include an empty character. For example, a gene name "k4" could occur in a journal article as "kinin 4 (k4)". It was therefore important to define several characters as substitutes for a space character. The alphabet in Appendix E defines the nucleotide combination ATCC as such a substitute.

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using a Perl-script (see Appendix F). The script shown in Appendix G scans the output file, which is sometimes several megabytes long, for any segments that start at position 1 of the database sequence (thus disregarding any segments that are only part of the sequence). In addition, the script allows for 10% mismatches between the aligned sequences for long sequences (as shown in the script of Appendix E), or 0% mismatches for short sequences. After scanning the output file, an intermediary file that lists the candidate sequences is created:

tran|365|381|gp|18493 tran|1|17|gp|18493 10 peci|549|565|gp|58106 il-2|621|637|gp|82396 il-2|325|341|gp|82396 gati|193|209|gp|92088 prod|641|657|gp|52292 15 rap1|105|121|gp|49898 spec|545|561|gp|33183 crip[385[401|gp[118905 crip|21|37|gp|118905 as|161|177|gp|133961 20 her|65|77|gp|88411

The intermediary file lists the name of the sequence, followed by the starting and end point in the query sequence (corresponds to where the two sequences matched), the semantic class of the name (protein, gene or protein/gene). The last number is not considered.

25 The intermediary file is then scanned by another Perl program

(Appendix G). This program compares the starting end points with the actual text,
making sure that the matched name is an 'autonomous' entity in the query text. For
example, while "per" in " per gene" should be recognized as a gene name, "per" in
"personal" should not be recognized as a gene name. The program recognizes other

30 characters than the space character delimiting an 'autonomous' gene or protein name.

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the absence of costimulation, T cells activated through their antigen ..." is translated into

A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. The query is executed using the blastall program that is included in the BLAST package. The query line looks like:

blastall -p blastn -d FASTA.dat -i query.txt

The flag 'p' denotes the sub-program (blastn is a sub-program of blastall that performs nucleotide matches), 'd' denotes the file that contains the FASTA entries and 'i' denotes the translated query text.

Significant alignments associated with gene and protein names are listed in the BLAST output file. This is an excerpt from a BLAST output file:

gi|63624 species,gp,ner

20 Length = 12

Score = 24.4 bits (12), Expect = 3e-05

Identities = 12/12 (100%)

Strand = Plus / Plus

Query: 729 acagaacgacct 740

Sbjct: 1 acagaacgacct 12

The first line denotes the database entry. The second line denotes the database sequence length, followed by the alignment score and the E-value. The next line indicates paired matches, mismatches and gapped alignment (the latter two are not shown in this example). The lines 'Query' and 'Sbjct' show the actual alignment between the query and database sequence. This output file is subsequently processed

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hox al wac 3'-end pit-1/ghf-1 variant [...]

This list of gene and protein names is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The conversion chart is listed in Appendix E. The encoded names are then imported into the BLAST database using the FASTA format. For example, the first entry in the list above is "gfap gamma." After translation using the conversion chart, the same name appears as follows:

AGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

Thus, the complete FASTA entry looks like this:

>gi|1 species,gp,gfap gamma

AAGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

In FASTA, the definition line (marked with '>') contains information about the database entry. This line can contain any kind of information. The information important for this particular example is the third entry in the definition line, 'gp', that specifies that the name can represent a gene or a protein. If the name is unambigous, then the definition line states that the name is only associated with a gene ('g') or protein ('p'). The fourth entry in the definition line is the name of the protein or gene, "gfap gamma" in this case.

The second line in the FASTA format normally contains the actual sequence of the protein/gene. In the example presented, the second line contains the translated protein or gene name.

All gene and protein names are translated into the nucleotide representation and converted into the FASTA format. Then, the database containing these FASTA entries are specially compiled for use in BLAST queries using a program that is included in the BLAST package called "formatdb".

Thus, the scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. For example, the sentence "In

signifying that the agent has not been specified; the second argument is a protein with the value jnk. The second argument is the target:

[action,inactive,[protein,bad],[action,phosphorylate,x,[protein,jnk]
In summary, a computer system has been disclosed that generates
structured information concerning protein and gene interactions and relationships.

5.2. USE OF BLAST FOR FINDING GENE AND PROTEIN NAMES IN JOURNAL ARTICLES

In a specific embodiment of the invention, an exhaustive list of gene and protein names, extracted from GeneBank, is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The encoded names are then imported into the BLAST database using the FASTA format. The scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. Significant alignments associated with gene and protein names are listed in the BLAST output file, which is subsequently processed using Perl-scripts. The final result consists of the original journal article with XML tags surrounding the gene and protein names.

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names. In addition, in order to fine-tune the matching process, different BLAST parameters were adjusted, such as the word size (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs) and mismatch penalty (exact vs approximate matching).

In a specific embodiment of the invention, gene and protein names are extracted from GeneBank's gene symbol index file. The following is an excerpt of the file after discarding entries that are either composed of only numbers or of less than two alphabetic letters:

gfap gamma

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repeated until an analysis of each segment is obtained or until segmenting is no longer possible.

Mode 3 requires a well-formed pattern for the "largest" prefix of the segment, *i.e.*, usually at the beginning of the segment. This occurs when a sentence contains a pattern at the end which is not in the grammar but a beginning portion that is included. For example, in "bad inactivates jnk at this time", the beginning of the sentence "bad inactivates jnk" will be parsed and the remainder will be skipped.

Mode 4 requires that undefined words be skipped and an analysis be attempted in accordance with Mode 1. Mode 4 is useful where there are typographical errors and unknown words. For example, in the phrase "abc bad inactivates jnk", the word abc is unknown to the system and will be ignored but the remainder of the phrase will be parsed.

Mode 5 first requires that the first word or phrase in the segment associated with an action be found. Next, an attempt is made to recognize the phrase starting with the leftmost recognizable argument. For example, in "during bad inactivates jnk on the fifth day," the phrase "bad inactivates jnk" will be parsed and the remaining words will not be. If no analysis is found, recognition is retried at the next possible argument to the right. This process continues until an analysis is found.

Process_sects with *get_section* and *parse_sentences* gets each section and generates intermediate output for the sentences in each section.

Write produces the output as a list consisting of relations and interactions

Setargs sets arguments or parameter values based on user input or by default.

25 The structured output generated by the GENIE program uses a frame-based representation. Each frame specifies the informational type, the value, and arguments or modifier slots which are also frames. Consider the text data input "bad inactivates the phosphorylation of jnk." A corresponding output, as shown below, is a frame denoting an action, which has the value inactivate; in addition, there are two arguments. The first argument is a protein bad and the second argument is an action with the value phosphorylate, which has two arguments. The first argument is x

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mode) and Protocol (html or plain). *Process_sents* is called by another predicate, after user-specified parameters have been processed.

The parsing modes are selected by GENIE so as to parse a sentence or phrase structure using a grammar that includes one or more patterns of semantic and syntactic categories that are well-formed. For example, for the phrase "bad inactivates ink", a legitimate pattern can be substance1 action substance2, wherein substance1 = protein bad, action = "inactivates" and substance2 = "jnk." However, if parsing fails, various error recovery modes are utilized in order to achieve robustness. The error recovery techniques use methods such as segmenting the sentence, processing large chunks of the sentence, and processing local phrases. Each recovery technique is likely to increase sensitivity but decrease specificity and precision. Sensitivity is the performance measure equal to the true positive rate of the natural language processing, i.e., the ratio of information extracted by the natural language processing system that should have been extracted. Specificity is the performance measure equal to the true negative information rate of the system, i.e., the ratio of information not extracted by the NLP system that should not have been extracted. Precision is the reliability of the system, i.e., the ratio of information extracted correctly compared to all the information that was extracted. In processing a report, the most specific mode is attempted first, and successive less specific modes are used only if needed.

In accordance with the preferred embodiments of the present invention, the parser of Figure 2 includes five parsing modes, Modes 1 through 5, for parsing sentences or phrases. Nominally, the parser is configured to first select Mode 1. If Mode 1 is not possible, the program continues with Mode 2 and so forth until parsing is complete. With Mode 1, the initial segment is the entire sentence and all words in the segment must be defined. This mode requires a well-formed pattern for the complete segment.

Mode 2 requires that the sentence or phrase be segmented at certain types of words or phrases, e.g., " is attributable to." Here, an attempt is made to recognize each segment independently, i.e., a first segment ending with the word "is" and a second segment beginning with the word after "to." The segmenting process is

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formed syntactic and semantic patterns in the sentence and to generate structured output forms. The parser proceeds by starting at the beginning of the sentence element list and following the grammar rules. When a semantic or syntactic category is reached in the grammar, the lexical item corresponding to the next available unmatched element is obtained and its corresponding lexical definition is checked to see whether or not it matches the grammar category. If it does match, the word or phrase is removed from the unmatched sentence list, and the parsing proceeds. If a match is not obtained, an alternative grammar rule is tried. If no analysis can be obtained, an error recovery procedure is followed so that a partial analysis is attempted. The actual grammar used for GENIE appears as Appendix D.

The parser module of GENIE uses the lexicon, and a grammar module to generate target forms. Thus, in addition to parsing of complete phrases, subphrase parsing can be used to an advantage where highest accuracy is not required. In case a phrase cannot be parsed in its entirety, one or several attempts can be made to parse a portion of the phrase for obtaining useful information in spite of a possible loss of information.

Conveniently, each module is software-implemented and stored in random-access memory of a suitable computer, e.g., a work-station computer. The software can be in the form of executable object code, obtained, e.g., by compiling from source code. Source code interpretation is not precluded. Source code can be in the form of sequence-controlled instructions as in Fortran, Pascal or "C", for example. Alternatively, a rule-based system can be used such a Prolog, where suitable sequencing is chosen by the system at run-time.

An illustrative portion of the GENIE system is shown in the Appendix D in the form of a Prolog source listing with comments. The following is further to the comments.

Process_sents with get_inputsents, process_sects and outputresults reads in an input stream, processes sections of the input stream according to parameter settings, and produces output according to the settings, respectively. Among parameters supplied to Process_sents are the following: Mode (specifying the parsing

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syntactic and semantic. The syntactic lexicon for actions specifies the main syntactic category such as "v" for verb, "ving" for progressive form of verb, and "activation" for noun. The semantic entries for actions not only categorize the actions, but also specify features for each action. For example, one feature provides the number of arguments that are expected for the action, *i.e.*, some actions are associated with two arguments because they have an agent and a target as "inactivate", and others just have an agent "mutate." The lexicon of substances and structures appears as Appendix A; the syntactic lexicon for actions appears as Appendix B; and the semantic lexicon of actions appears as Appendix C.

A second feature specifies whether or not the arguments should be reversed when obtaining the target form. For example the arguments of "attributable to" should be reversed, *i.e.*, in "the phosphorylation of jnk is attributable to the activation of bad", the underlying action is "cause" (from "attributable to"), the agent is the "activation of bad" and the target is "the phoshorylation of jnk"), whereas the arguments of "activates" is not (i.e. in "jnk activates bad", the agent is "jnk" and the target is "bad").

Figure 2 shows a preprocessor module of GENIE by which natural-language input text is received. The preprocessor thus performs lexical lookup to identify and categorize multi-word and single word phases within each sentence. The output of this component consists of a list of word elements where each element is associated with a word or multi-word phrase in the report. For example, assuming that the sentence "bad functions as a negative regulator of the activation of jnk" is at the beginning of the report, it would be represented as a list of elements where each element is a word or phrase. For example, element 1 is associated with "bad", element 2 with the multi-word phrase "functions as a negative regulator of", element 8 with "the", and element 9 with "activation". The remainder of the list of word positions would be associated with the remaining words in the report. Some of the phrases may not need lexical lookup because they already have been tagged by a previous component. Such a tagging system is described below in Section 5.2.

The second component of the GENIE system is the parser. It utilizes the grammar and categories assigned to the phrases of a sentence to recognize well-

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A natural-language phrase included in text document is understood as a delimited string comprising natural-language terms or words. The string is computer readable as obtained, e.g., from a pre-existing database, a keyboard input, optical scanning of typed or handwritten text, or processed voice input. The delimiter may be a period, a semicolon, an end-of-message signal, a new-paragraph signal, or any other suitable symbol recognizable for this purpose. Within the phrase, the terms may be separated by another type of delimiter such as a blank or another suitable symbol.

As a result of phrase parsing, terms in a natural-language phrase are classified, (e.g., as referring to a gene, a protein, or their interactions) and the relationships between the interactions are established and represented in a standard form. For example, in the sentence "Rap inhibited fyn", the structured form would be:

[action,inactivate,[protein,rap],[protein,fyn]].

In such an example, the interaction is "inactivate", the agent is "Rap" and the target is "fyn." More complex sentences consisting of nested relationships, such as "The activation of BAD was suppressed by the phosphorylation of JNK" can also be parsed and represented appropriately. The structured output form for this sentence would be: [action,inactivate,[action,phosphorylate,x,[protein,jnk],[action,activate,x,[protein,bad]]

In the first example, the primary interaction is "inactivate"; in the second example, an interaction "phosphorylate" is the agent where the protein "jnk" is its target (the agent of "phosyphorylate" in not specified and thus is represented as "x"). In this example, the target of "inactivate" is also an interaction "activate" where the target is the protein "bad" and the agent is unknown.

While parsing is based on both syntactic and semantic grammatical patterns, the substances in a domain are normally only semantic categories such as "protein", "gene", and "small molecule." There are no corresponding syntactic categories needed for these substances because they are normally all nouns. However, each action can be categorized both semantically and syntactically. An action, which is a semantic category, can generally occur syntactically as a verb "inactivate" or as a noun "inactivation." Therefore there are two sets of lexical entries for the actions:

5.1. THE NATURAL LANGUAGE PROCESSING

The present invention relates to a natural language processing system that is designed to parse the electronic versions of articles published in journals that report on structural interactions among genes and proteins. The system provides a method for extracting information on interactions among genes and proteins, their domain/motif structure, and/or their sub-cellular and tissue expression/distribution patterns, followed by computer representation of such information.

The general natural language-processing system of the invention is schematically depicted in Figure 2. The collection phase automatically collects articles from appropriate literature, and selects articles that contain relevant information using Keyword search techniques. In the next phase, the preprocessor standardizes the selected articles so that they consist of tagged ASCII text where the tags delineate critical components of the article. The next phase, termed the extraction phase, retrieves and classifies biological entities, *i.e.*, as names of proteins, genes and small molecules. In addition, the relationship extraction phase recovers structural relationships between the entities. This phase is followed by a phase which performs an analysis of the sequence of events.

The final phase of the system processes the output extracted from an article to remove redundancies, inconsistencies and to incorporate implicit information before adding the extracted knowledge consisting of biological entities, their attributes, conditional constraints, and relationships between them, for subsequent use in analysis and hypothesis testing. The information extraction system as depicted in Figure 2, referred to herein as "GENIE," is designed for use as a general processor within the domain of genomics literature although the system may also be used in other specialized domains. GENIE is an adaptation of MedLEE developed for the medical domain. GENIE uses the same source code as MedLEE but the Lexicons and grammar were adapted for genomics literature.

The information extraction system of the present invention is described below, by way of example, with reference to the genomics domain uses of GENIE. It is written in Quintus Prolog and uses the Unix or Windows operating systems, as described in detail below.

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Figure 17B. Nucleotide sequence of the human Mad3 gene.

Figure 17C. Complete sequence of the human Mad3 protein. A search was conducted to identify overlapping sequences. The complete sequence of the gene was assembled and the amino acid sequence deduced. The translated human Mad3 sequence consists of 206 amino acid residues 81% of which are identical to the mouse Mad3 protein.

Figure 17D. Multiple alignment of the human Mad3 amino acid sequence with known Mad proteins.

Figure 18A. Phylogenetic tree indicating relationship between three known mouse Mad genes and their two human homologs.

Figure 18B. Phylogenetic tree including new human Mad3 sequence.

The phylogenetic tree indicates that the new human gene belongs to the family of Mad proteins and is an ortholog of mouse Mad3.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods for identification of novel genes comprising: (i) generating specialized databases containing information on gene/protein structure, function and regulatory interactions and, (ii) sequence analysis which includes homology searches and motif analysis thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The specialized databases are constructed utilizing information concerning gene/protein structure or function derived from unpublished data, research articles and/or existing databases. The specialized databases can be used to identify novel genes by: (i) searching for motif/domain combinations characteristic for a putative gene of interest; (ii) phylogenetic tree analysis of homologous genes for predicting the existence of yet undiscovered genes; (iii) comparing members of interactive gene/protein networks from different species for predicting the existence of yet undiscovered genes; and (iv) testing a hypothesis with regard to known interactions of homologs from other species in regulatory pathways.

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Figure 11A and 11B are diagrams respectively representing hypothetical examples of evaluating the impact of a "knockout" of hypothetical gene A on the expression of a hypothetical gene B. The effect of knock-out of gene A calculated by multiplication along the shortest pathway connecting genes A and B is inhibition of gene B, the resulting effect being zero if the orientation of only one arc in the same pathway is reversed;

Figure 12 is a flow chart representing the scheme of gene discovery analysis involving motif/domain analysis in accordance with the present invention; and

Figure 13 Identification of genes in *C. elegans* containing either POZ or kelch domains. The protein excession numbers are indicated adjacent to the different protein domains. The protein corresponding to accession number gi/1132541 contains a POZ domain, death domain, kinase domain and heat repeat.

Figure 14A. Two human sequences with the closest homology to the C. elegans sequence gi/1132541.

Figure 14B. Computed gene tree indicating that the identified human gene represents an ortholog of the *C. elegans* gene gi/1132541.

Figure 14C. Nucleotide sequence of the death domain gene.

Figure 14D. Deduced amino acid sequence of the death domain

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Figure 15. Identification of candidate gene implicated in the etiology of Chronic Lymphocytic Leukemia (CLL). Sequence homology between a CLL region open reading frame and mouse Rpt1 (sp/P15533/RPT1) is presented.

Figure 16A-B. Model of regulatory functions of Rpt1. Figure 16A indicates that in mouse T lymphocytes Rpt1 serves as a repressor of the gene for interleukin 2 receptor (IL-2R). Figure 16B demonstrates that when Rpt1 is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway for T-lymphocytes resulting in accumulation of T-lymphocytes in blood.

Figure 17A. Two EST sequences identified by searching a protein dbEST using the mouse Mad3 protein as a query.

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is a graph depicting a history of a few genes from the same species, where each species can be represented by multiple paralogous genes (because the set of known genes is incomplete for most genomes, and there are often multiple representations of the same gene family in the same genome, the gene tree can be drastically different from the corresponding species tree); and a "reconciled tree", which is the gene tree that would be obtained if gene deletions were completely forbidden and all genes were known for all species under analysis;

Figure 6 shows the original tree of ALDH sequences, indicating sequence clusters where bacterial, plant, fungal and nematode orthologous genes are present, but a human ortholog was not yet known;

Figure 7 shows the same phylogenetic tree as in Figure 6 with an additional human protein, referred to as antiquitin which was discovered by the method of the invention:

Figure 8 is a schematic diagram illustrating functional network-based gene discovery in accordance with the present invention;

Figure 9A presents diagrams depicting the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. Proteins in different species denoted with the same numeral are considered orthologous. The diagrams show that regulatory relationships between a pair of proteins can be of three different kinds;

Figure 9B, 9C, and 9D are diagrams representing Boolean operations OR, AND, and XOR, on arcs of the two oriented graphs of Figure 9A, the same operations being applicable to the set of vertices of the two oriented graphs;

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (1 and 2) for species A and three hypothetical proteins (1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ε, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ε, respectively. The motif analysis can indicate that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A;

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predict undiscovered genes. This program also includes a set of tools for generating motif/domain models from multiple sequence alignments of known genes and for using these models for extraction of structurally and/or functionally homologous sequences from databases which contain raw sequence data.

The invention further provides for a simulation and hypothesis testing program which relies on the specialized databases of gene/protein interactions for identifying potentially undiscovered members of multigene families through comparisons of regulatory networks for different species and testing hypotheses with regard to regulatory cascades. A comparison of homologous regulatory networks within the same organism and between different species of organisms will allow the identification of genes absent in one of the systems under comparison, thus providing a set of candidate genes. In this way, genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified, mapped and subjected to mutational analysis and functional studies.

4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a block diagram illustrating the three major programs of the method according to the present invention: (i) the generation of specialized databases based on information on gene/protein structure, function and regulatory interactions derived from research papers and databases; (ii) sequence analysis; and (iii) simulation and hypothesis testing;

Figure 2 is a block diagram of an information extraction system in accordance with a preferred embodiment of the present invention;

Figure 3 is a diagram illustrating the object representation of molecules and relations between them;

Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways, these keywords having been utilized for generating a specialized sequence database Apoptosis3, this list having been compiled manually for testing the concept of specialized databases;

Figure 5 shows a "species tree," which is a graph depicting the correct order of speciation events leading to a set of present day species; a "gene tree," which

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3. SUMMARY OF THE INVENTION

In accordance with the present invention there is provided methods for identification of novel genes comprising (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The invention is based, in part, on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, by comparing phylogenetic trees or regulatory networks and identifying genes and/or proteins absent in one system under comparison, the existence of as yet unidentified genes and/or proteins can be predicted. To make meaningful comparisons of phylogenetic trees it is necessary to distinguish between orthologs and paralogs. The present invention provides a method useful for discriminating between orthologs and paralogs and inferring the existence of as yet unidentified genes and/or proteins.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. Specifically, the natural language processing system of the invention is used to parse the articles published in biological journals focusing on structure and interactions among genes and proteins followed by computer representation of such interactions.

In accordance with the present invention, specialized databases are developed that contain information on gene/protein structure and interactions based on information derived from preexisting databases and/or research articles including information on interactions among genes and proteins, their domain/motif structure and their subcellular and tissue expression/distribution patterns.

The invention relates to a sequence analysis program which utilizes the specialized database for comparison of a single sequence, processing the output into a sequence alignment, computing phylogenetic trees, and analyzing these trees to

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Two homologous genes taken from different species that originate from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originate from a common ancestor via a series of events involving intragenomic duplications are call paralogs. Tatusov et al. (1994, Proc. Nat.l, Acad. Sci USA 91:12091-12095) describe comparisons of proteins encoded by the genomes of different phylogenetic lineages and elucidation of consistent patterns of sequence similarities permitting the delineation of clusters of orthologous groups (COGs). Each COG consists of individual orthologous genes or orthologous groups of paralogs from different phylogenetic lineages. Since orthologs typically have the same function, the classification of known genes and proteins into clusters of orthologous groups permits the assignment of a function to a newly discovered gene or protein by merely classifying it into a COG. Although Tatusov describes a method for assigning a function to a newly discovered gene, he does not describe a method for predicting the existence of undiscovered genes. In addition, Yuan, et al. attempted simultaneous reconstruction of a species tree and identification of paralogous groups of sequences and detection of orthologs in sequence databases (Yuan et al., 1998, Bioinformatics 143:285-289).

Other groups have aimed at capturing interactions among molecules through the use of programs designed to compare structures and functions of proteins 20 (Kazic 1994, In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494; Kazic, 1994, In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140; Goto et al., 1997, Pac. 25 Symp. Biocomput. p. 175-186; Bono et al., 1998, Genome Res. 8:203-210; Selkov et al., 1996, Nucleic Acids Res. 24:26-28). These projects are significantly different from the inventive methods described herein because they do not describe methods for deducing the existence of as yet unknown genes based on comparisons of regulatory pathways and gene structure between one or more species. The present invention 30 provides a method for increasing the sensitivity of analysis methods through the generation of specialized databases.

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loci, can hardly be found using this strategy because of the complications associated with multiple loci linkage analysis.

Specialized databases for homology searches have also been utilized in disease gene discovery projects. In recent years a number of efficient sequence comparison tools have been developed such as the BLAST (Basic Local Alignment Search Tool) family of programs designed for comparison of a single "search sequence" with a database (see Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), the family of Hidden Markov Model methods for comparison of a set of aligned sequences that usually represent a protein motif or domain with a database (e.g., Krogh et al., 1994, J. Mol. Biol. 235:1501-1531; Grundy et al., 1997, Biochem Biophys. Res. Commun. 231:760-6) and various other comparison tools (Wu et al., 1996, Comput. Appl. Biosci 12:109-118; Neuwald et al., 1995, Protein Sci. 4:1618-1632; Neuwald, 1997, Nucleic Acids Res. 25:1665-1677).

When used in disease gene discovery projects, homology searches can be enhanced by creating specialized databases that utilize statistical analysis for evaluating significance of sequence similarities in comparison of new sequences with a database of known sequence. Such databases are fine-tuned to the size of the database used (Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), so that the same level of homology between a search sequence and a database sequence can be determined to be highly significant if the search sequence is compared with a smaller database, or insignificant and thus undetectable, if the search sequence is compared with a larger database.

In alternatives to standard homology searches, in projects oriented towards gene discovery, researchers usually have some *a priori* knowledge about the set of genes/proteins that might display important similarity to the unknown new gene. Therefore, selecting an *a priori* defined set of genes/proteins for comparison with new experimental sequences is a feasible and useful strategy. This strategy was successfully applied to search for homologs of disease genes in yeast and nematode genomes by Mushegian et al. (1997, Proc. Natl. Acad. Sci USA 94:5831-5836).

2.2. IDENTIFICATION OF NOVEL GENES

A variety of different methods are currently utilized for the identification and characterization of novel genes. Perhaps the most widely used method for generating large quantities of sequence information is via high throughput nucleotide sequencing of random DNA fragments. A disadvantage associated with this gene discovery technique is that in most instances when genes are identified their function is unknown.

For identification of specific disease genes, positional cloning is currently the most widely used method. The positional cloning approach combines methods of formal genetics, physical mapping and mutation analysis and usually starts with a precise description of the disease phenotype and a tracing of the disease through families of affected individuals. Genetic linkage data obtained from the analysis of affected families frequently allows the determination of an approximate genomic localization of the candidate disease gene with a precision of several millions of nucleotides. Once localized, the genetically defined chromosomal region is then recovered from genomic libraries as a contiguous set of genomic fragments. Genes residing in the disease-related region are determined by analysis of transcripts that are transcribed from the genomic fragment. From this analysis an initial set of candidate genes for a particular disease are identified based on the presence of the gene product in the biological system affected by disease and a correlation between its expression pattern and the pattern of disease progression.

Important information for selection of candidate genes also comes from analysis of their homology with genes known to be part of the same or related biological system. Finally, the ultimate proof of association between a gene and a genetic disorder comes from mutational analysis of a gene in patients affected by the disorder and from demonstration of a statistical correlation between occurrence of mutation and the disease phenotype.

Although positional cloning is a powerful method for gene discovery, 30 the experimental method is extremely tedious and expensive. Moreover, disease genes implicated in genetically complex disorders, *i.e.*, those controlled by multiple

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Natural language processing is an automated system that provides for a complex of programs for automatic retrieval of information from text analysis and for the computer representation of that information in a form that allows efficient access and extraction of that information. MedLee (Medical Language Extraction and Encoding System) has recently been successfully used for processing different types of medical texts as described in co-pending United States Patent Application Serial Number 09/370,329, incorporated herein in its entirety by reference (see also, Friedman et al., 1994, J. Amer. Med. Inf. Assoc. 1:161-174; Hripcsak et al. 1995, Ann. Intern. Med. 122:681-688; Hripcsak et al., 1998, Meth. Inform. Med.; Jain et al., 1996, Proc. AMIA Annu. Fall Symp. 542-546; Knirsch et al., 1998). When tested, MedLEE was on average as successful in retrieving reports associated with specified clinical connections as twelve medical experts invited for evaluation of the system.

Another text analysis technique has recently been developed that combines finite-state machines with statistical machine learning approaches. These models extract detailed semantic information from texts (e.g., see Hatzivassiloglou 1996, In Klavens, J.L., and Resnick, P.S. (eds) *The Balancing Act: Combining Symbolic and Statistical Approaches to Language*, MIT Press, Cambridge, MA) when extensive prior knowledge about the domain is not available. The techniques have been subsequently applied to the tasks of (i) automatically identifying medical terms for the automated summarization of research articles reporting on clinical studies and (ii) sanitizing sensitive information in patient records so that they can be widely disseminated for research purposes.

A number of projects have also been developed as statistical information extraction tools that operate with limited or no prior knowledge about the application domain. These earlier efforts include XTRACT, a tool that recovers collocational restrictions between words that has been licensed to more than thirty sites worldwide (Smadja, F., 1993, J. Comp. Ling. 19:143-177), CHAMPOLLION, a system that retrieves bilingual mappings between words and phrases in parallel texts from different languages (Smadja, F. et al. 1996, J. Computational Linguistics 22:1-38), and a system that automatically aligns noisy, semi-parallel texts from different languages (Fung, P. and McKeown, K.R., 1997, Machine Translation 11:23-29).

in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications. Specifically, the present invention provides for the generation of specialized databases containing information on gene/protein structure, function and regulatory interactions based on the retrieval of such information from research articles and databases, and computer representation of such information in a manner that allows efficient access to the extracted information.

The invention further provides for the use of the specialized databases for identifying novel genes based on detection of sequence similarities and domain/motif matches between genes/proteins, computation and interpretation of phylogenetic trees for multigene families, and analysis of homologous regulatory networks. The methods of the invention are based on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, a comparison of homologous/similar networks within the same organism and between different species will allow the identification of genes absent in one of the systems under comparison. In this way genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified.

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2. BACKGROUND OF THE INVENTION

2.1. <u>NATURAL LANGUAGE PROCESSING</u>

Researchers working in molecular biology must constantly consider the information present in the literature relating to their regulatory systems of interest and the genes and proteins that operate within those systems. Unfortunately, to remain upto-date on the relevant literature, the researcher is required to perform laborious reading and manual integration of research articles, each of which may address a narrow subject. Therefore, technology that enables rapid retrieval of information from literature and manipulation of derived functional data should have a dramatic effect on the accesses of the researcher to important facts and ultimately should facilitate the discovery of novel human genes.

GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

SPECIFICATION

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The invention described herein was funded in part by a grant from the National Library of Medicine, namely, Grant Number's LM06274 and LM05627. The United States Government may have certain rights to the invention. The present specification contains a computer program listing which appears as a microfiche Appendix H.

STATEMENT REGARDING MATERIAL SUBJECT TO COPYRIGHT

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An appendix containing source code listing utilized in practicing an exemplary embodiment of the invention is included as part of the Specification.

1. INTRODUCTION

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The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7:	<u> </u>	(1	1) International Publication Number:	WO 00/63687
G01N 31/00, G06F 15/00, 17/00		(43) International Publication Date:		26 October 2000 (26.10.00)
(21) International Application Number: PCT/US	00/103	02	(81) Designated States: AE, AG, AL,	AM, AT, AU, AZ, BA, BB,

14 April 2000 (14.04.00)

(30) Priority Data:

(22) International Filing Date:

60/129,469 15 April 1999 (15.04.99) US 09/327,983 8 June 1999 (08.06.99) US

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81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.

(54) Title: GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATION-SHIPS AMONG KNOWN GENES AND PROTEINS

(57) Abstract

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest. The present invention also relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications.

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synw(instigating, ving).
synw(instigation,n).
synw(interact, v).
synw(interact, vp).
synw(interacted, ved).
synw(interacted, ven).
synw(interacting,n).
synw(interacting, ving).
synw(interaction,n).
synw(interactions,n).
synw(interacts, vp).
synw(join ,vp).
synw(join, v).
synw(joined, ved).
synw(joined, ven).
synw(joining,n).
synw(joining, ving).
synw(joins, vp).
```

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synw(juncture, n).
synw(liberate, v).
synw(liberate, vp).
synw(liberated, ved).
synw(liberated, ven).
synw(liberates, vp).
synw(liberating,n).
synw(liberating, ving).
synw(liberation,n).
synw(limit, v).
synw(limit, vp).
synw(limitation, n).
synw(limited, ved).
synw(limited, ven).
synw(limiting,n).
synw(limiting, ving).
synw(limits, vp).
synw(link,n).
syrw(link,v).
synw(link, vp).
synw(linked, ved).
synw(linked, ven).
synw(linking,n).
synw(linking, ving).
synw(links, vp).
synw(mediate, v).
synw(mediate, vp).
synw(mediated, ved).
synw(mediated, ven).
synw(mediates, vp).
synw(mediating,n).
synw(mediating, ving).
synw(mediation, n).
synw(methylate, vp).
synw(methylate, v).
synw(methylated, ved).
synw(methylated,ven ).
synw(methylates, vp).
synw(methylating,n).
synw(methylating, ving).
synw(methylation, n).
synw(modification,n).
synw(modified, ved).
```

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synw(modified, ven).
synw(modifies, vp).
synw(modify, v).
synw(modify, vp).
synw(modifying,n).
synw(modifying, ving).
synw(mutate, v).
synw(mutate, vp).
synw(mutated, ved).
synw(mutated, ven).
synw(mutates, vp).
synw(mutating,n).
synw(mutating, ving).
synw(mutation,n).
synw(overexpress, v).
synw(overexpress, vp).
synw (overexpressed, ved) .
synw(overexpressed, ven).
synw(overexpresses, vp) .
synw(overexpressing, n).
synw(overexpressing, ving).
synw(overexpression, n).
synw(pair,v).
synw(pair, vp).
synw(paired, ved).
synw(paired, ven).
synw(pairing,n).
synw(pairing, ving).
synw(pairs, vp).
synw(phosphorylate,n).
synw(phosphorylate, vp).
synw(phosphorylated, ved).
synw(phosphorylated,ven).
synw(phosphorylates,vp).
synw(phosphorylating,n).
synw(phosphorylating,ving).
synw(phosphorylation, n).
synw(promote, v).
synw(promote, vp).
synw(promoted, ved).
synw(promoted, ven).
synw(promotes, vp).
synw(promoting,n).
```

```
synw(promoting, ving).
synw(promotion, n).
synw(prompt,n).
synw(prompt, v).
synw(prompt, vp).
synw(prompted, ved).
synw(prompted, ven).
synw(prompting, n).
synw(prompting, ving)
synw(prompts, vp).
synw(react, v).
synw(react, vp).
synw(reacted, ved).
synw(reacted, ven).
synw(reacting,n).
synw(reacting, ving).
synw(reaction,n).
synw(reacts, vp).
synw(regulate, v).
synw(regulate, vp).
synw(regulated, ved).
synw(regulated, ven).
synw(regulates, vp).
synw(regulating,n).
synw(regulating, ving).
synw(regulation, n).
synw(release, n).
synw(release, v).
synw(release, vp).
synw(released, ved).
synw(released, ven).
synw(releases, vp).
synw(releasing, n).
synw(releasing, ving).
synw(removal, n).
synw(remove, v).
synw(remove, vp).
synw(removed, ved).
synw(removed, ven).
synw(removes, vp).
synw(removing,n).
synw(removing, ving).
synw(replace, v).
```

```
synw(replace, vp).
synw(replaced, ved).
synw(replaced, ven).
synw(replacement, n).
synw(replaces, vp).
synw(replacing,n).
synw(replacing, ving).
synw(repress, vp).
synw(repress, v).
synw(repressed, ved).
synw(repressed, ven) .
synw(represses, vp).
synw(repressing,n).
synw(repressing, ving).
synw(repression, n).
synw(require, v).
synw(require, vp).
synw(required, ved).
synw(required, ven).
synw(requirement, n).
synw(requires, vp).
synw(requiring,n).
synw(requiring, ving).
synw(restrain, vp).
synw(restrain, v).
synw(restrained, ved).
synw(restrained, ven).
synw(restraining,n).
synw(restraining, ving).
synw(restrains, vp).
synw(restraint, n).
synw(sensitization, n).
synw(sensitize, vp).
synw(sensitize, v).
synw(sensitized, ved).
synw(sensitized, ven).
synw(sensitizes, vp).
synw(sensitizing,n).
synw(sensitizing, ving).
synw(separate, v).
synw(separate, vp).
synw(separated, ved).
synw(separated, ven).
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```
synw(separates, vp).
synw(separating, n).
synw(separating, ving).
synw(separation, n).
synw(sever,v).
synw(sever, vp).
synw(severance, n).
synw(severed, ved).
synw(severed, ven).
synw(severing,n).
synw(severing, ving).
synw(severs, vp).
synw(signal, v).
synw(signal, vp).
synw(signaled, ved).
synw(signaled, ved).
synw(signaled, ven).
synw(signaling,n).
synw(signaling, ving).
synw(signals, vp).
synw(split,n).
synw(split,v).
synw(split, ved).
synw(split, ven).
synw(split, vp).
synw(splits, vp).
synw(splitting, n).
synw(splitting, ving).
synw(stimulate, v).
synw(stimulate, vp).
synw(stimulated, ved).
synw(stimulated, ven).
synw(stimulates, vp).
synw(stimulating,n).
synw(stimulating, ving).
synw(stimulation, n).
synw(substitute, v).
synw(substitute, vp).
synw(substituted, ved).
synw(substituted, ven).
synw(substitutes, vp).
synw(substituting,n).
synw(substituting, ving).
```

```
synw(substitution,n).
synw(suppress, vp).
synw(suppress, v).
synw(suppressed, ved).
synw(suppressed, ven)...
synw(suppresses, vp).
synw(suppressing,n).
synw(suppressing, ving).
synw(suppression, n).
synw(tie,n).
synw(tie, v).
synw(tie, vp).
synw(tied, ved).
synw(tied, ven).
synw(ties, vp).
synw(transcribe, v).
synw(transcribe, vp).
synw(transcribed, ved).
synw(transcribed, ven).
synw(transcribes, vp).
synw(transcribing,n).
synw(transcribing, ving).
synw(transcription,n).
synw(tying,n).
synw(tying, ving).
synw (ubiquitinization, n).
synw(ubiquitinize, v).
synw(ubiquitinize, vp).
synw(ubiquitinized, ved).
synw(ubiquitinized, ven).
synw(ubiquitinizes,vp).
synw (ubiquitinizing, n).
synw(ubiquitinizing, ving).
synw(urge, n).
synw(urge, v).
synw(urge, vp).
synw(urged, ved).
synw(urged, ven).
synw(urges, vp).
synw(urging, n).
synw(urging, ving).
% the following are verbs connected with complexes
synw(form, v).
```

```
synw(form, vp).
synw (forms, vp).
synw(formed, ved).
synw(formed, ven).
synw(forming,n).
synw(formation,n).
synw(assemble, v).
synw(assemble, vp).
synw(assembles, vp).
synw(assembled, ved).
synw(assembled, ven).
synw(assembling,n).
synw(assembly,n).
synw(dissassemble, v).
synw(dissassemble, vp).
synw(dissassembles, vp).
synw(dissassembled, ved).
synw(dissassembled, ven).
synw(dissassembling,n).
synw(dissassembly,n).
synw(dissociate, v).
synw(dissociate, vp).
synw(dissociates, vp).
synw(dissociated, ved).
synw(dissociated, ven).
synw(dissociating,n).
synw(dissociation,n).
synw(recruit, v).
synw(recruit, vp).
synw(recruits, vp).
synw(recruited, ved).
synw(recruited, ven).
synw(recruiting,n).
synw(recruitment,n).
```

```
% lexsemact.pat
% revised March 17, 2000
             SEMANTIC LEXICON OF ACTIONS
. 응응응응응응용
% For genomics - the grammar tests for semantic and syntactic cate
% separately for action type of categories; for substances the lex
ical
% entries are the same as in the medical area
% action type phrases have two entries: a semantic entry and a syn
tactic entry
% This lexicon contains the semantic entries for words and phrases
% semp is a lexical entry for phrasal lexicon
% semp(+Word1, +Sem, +Wordlist, +Targetform, +Features)
% semp specifies a semantic lexical definition for the genomics li
terature
% semp is equivalent to the predicate "phrase" in the medical area
% semp: Wordl is first word of phrase, Sem is semantic category
% semp: Wordlist is list of words in phrase, Targetform is output
form
% semp: Features is a list of 2 elements or the atom "def" represe
nting defaul
% semp: Features 1st element is rev or nrev meaning reversed or no
t reversed
% semp: Features 2nd element is a # specifying number of arguments
 for action
% semp: Features = def is equivalent to a list = [nrev,2]
% in case action has 1 argument, use [1,_]
%semw is a lexical entry for single word
% semw(+Word,+Sem,+Targetform,+Features)
% semw: the arguments are the same as for semp except there is no
Wordlist
응응응응응응응
 :- multifile(semp/5).
 :- multifile(semw/4).
semp(account, cause, [account, for], cause, [def]).
 semp(accounted, cause, [accounted, for], cause, [def]).
```

Appendix C
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semp(accounting, cause, [accounting, for], cause, [def]).
semp(accounts, cause, [accounts, for], cause, [def]).
           attach, [add, up], attach, [def]).
semp(added,
              attach, [added, up], attach, [def]).
semp(adds,
            attach, [adds, up], attach, [def]).
semp(are, cause, [are,a,means,of, producing], cause, [def]).
semp(are, cause, [are, due, to], cause, [2, rev]).
semp(as, cause, [as, a, result, of], cause, [2, rev]).
semp(attributable, cause, [attributable, to], cause, [2, rev]).
semp(attributed, cause, [attributed, to], cause, [2, rev]).
semp(based,cause,[based,on],cause,[2,rev]).
semp(based,cause,[based,upon],cause,[2,rev]).
semp(because, cause, [because, of], cause, [2, rev]).
semp(convey, signal, [conveys,a, signal], signal, [def]).
semp(conveyed, signal, [conveyed,a, signal], signal, [def]).
semp(conveying, signal, [conveying, a, signal], signal, [def]).
semp(conveys, signal, [conveys,a, signal], signal, [def]).
semp(dissociate, release, [dissociate, from], release, [def]).
semp(dissociated, release, [dissociated,from], release,[def]).
semp(dissociates, release, [dissociates, from], release, [def]).
semp(dissociation, release, [dissociation, from], release, [def]).
semp(down, signal, [down, '-', regulate], signal, [def]).
requlates B
                   A --> B
semp(down, signal, [down, '-', regulated], signal, [def]).
                                                                A down
                    A --> B
-regulates B
semp(down, signal, [down, '-', regulates], signal, [def]).
                                                                A down
-regulates B
                     A --> B
semp(down, signal, [down, '-', regulation], signal, [def]).
                                                                A dow
n-regulates B
                    A --> B
semp(due, cause, [due, to, the, fact, that], cause, [2, rev]).
semp(due, cause, [due, to], cause, [2, rev]).
semp(form, attach, [form, complex], attach, [def]).
semp(formation, attach, [formation, of, complex], attach, [def]).
semp(formed, attach, [formed, complex], attach, [def]).
semp(forms, attach, [forms, complex], attach, [def]).
semp(had, cause, [had, an, active, role, in], cause, [def]).
semp(has, cause, [has, an, active, role, in], cause, [def]).
semp(have, cause, [have, an, active, role, in], cause, [def]).
semp(is, cause,[is,a,means,of, producing],cause,[def]).
semp(is, cause, [is, due, to], cause, [2, rev]).
semp(functions, inactivate, [functions, as, a, negative, regulator, of], i
nactivate, [def]).
semp(function,inactivate,[function,as,a,negative,regulator,of],ina
```

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ctivate, [def]).
semp(lead, cause, [lead, to], cause, [def]).
semp(lead, cause1, [lead, to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leads, cause, [leads, to], cause, [def]).
semp(leads, cause1, [leads, to], cause, [def]).
semp(led, cause, [led, to], cause, [def]).
semp(may, cause, [may, be, responsible, for], cause, [def]).
semp(mediate, signal, [mediate, a, signal], signal, [def]).
                                                                 %À
mediates a signal to B
semp(mediated, signal, [mediated, a, signal], signal, [def]).
A mediates a signal to B
semp(mediates, signal, [mediates, a, signal], signal, [def]).
A mediates a signal to B
semp(mediation, signal, [mediation, of, a, signal], signal, [def]).
    %A mediates a signal to B
semp(n, createbond, [n,'-',acetylate],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylated],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylates],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylation],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acylate],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylated],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylates],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylation],'N-acylate',[def]).
semp(n, createbond, [n,'-',glycosylate],'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylated],'N-glycosylate', [def]).
semp(n, createbond, {n,'-',glycosylates},'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylation],'N-glycosylate',[def]).
semp(n,breakbond,[n,'-',terminal,proteolysis],'n-terminal proteoly
sis',[def]).
semp(o, createbond, [o,'-',glycosylate], '0-glycosylate',[def]).
semp(o, createbond, [o,'-',glycosylated], 'O-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylates], 'O-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylation], 'O-glycosylate',[def]).
semp(only,time,[only,after],'only after',[2,rev]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylate],
                   'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylated],
                     'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylates],
                'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylation],
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```
'prolyl-4-hydroxylate', [def]).
semp(result, cause, [result, from], cause, [2, rev]).
semp(result, cause, [result, in], cause, [def]).
semp(resulted, cause, [resulted, from], cause, [2, rev]).
semp(resulted, cause, [resulted, in], cause, [def]).
semp(resulting, cause, [resulting, from], cause, [2, rev]).
semp(resulting, cause, [resulting, in], cause, [def]).
semp(results, cause, [results, from], cause, [2, rev]).
semp(results, cause, [results, in], cause, [def]).
semp(set, release, [set, free], release ,[def]).
semp(set, release, [set, free], release ,[def]).
semp(sets, release, [sets, free], release, [def]).
semp(setting, release, [setting, free], release ,[def]).
semp(suppress, inactivate, [suppress, activity, of], inactivate, [
def]).
semp(suppressed, inactivate, [suppressed, activity, of], inactivat
e, [def]).
semp(suppresses, inactivate, [suppresses, activity, of], inactivat
e, {def}).
semp(suppression, inactivate, [suppression, of, activity, of], inac
tivate, [def]).
semp(switch, activate, [switch, on, the, activity, of],
, [def]).
semp(switched,
                 activate, [switched, on, the, activity, of],
vate, [def]).
semp(switches,
                 activate, [switches, on, the, activity, of],
vate, [def]).
semp(up, signal, [up, '-', regulate], signal, [2, rev]). % A up-regul
ates B B --> A
semp(up, signal, [up, '-', regulated], signal, [2, rev]).
semp(up, signal, [up, '-', regulates], signal, [2, rev]).
semp(up, signal, [up, '-', regulation], signal, [2, rev]).
semp(was, cause, [was,a,means,of, producing], cause, [def]).
semp(was, cause, [was, due, to], cause, [2, rev]).
semp(were, cause, [were,a, means, of, producing], cause, [def]).
semp(were, cause, [were, due, to], cause, [2, rev]).
semw(acetylate, createbond, acetylate,[def]).
semw(acetylated, createbond, acetylate,[def]).
semw(acetylates, createbond, acetylate,[def]).
semw(acetylation, createbond, acetylate,[def]).
semw(activate, activate, activate, [def]).
semw(activated, activate, activate, [def]).
semw(activates, activate, activate, [def]).
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```
semw(activation, activate, activate, [def]).
semw(add, attach, attach, [def]).
semw(added, attach, attach, [def]).
semw(addition, attach, attach, [def]).
semw(adds, attach, attach, [def]).
semw(after, time, after, [2, rev]).
                                    % temporal relations
semw(aggregate ,attach,attach,[def]).
semw(aggregated ,attach,attach,[def]).
semw(aggregates, attach, attach, [def]).
semw(aggregation ,attach,attach,[def]).
semw(arrest, inactivate, inactivate, [def]).
semw(arrested, inactivate, inactivate, [def]).
semw(arrests, inactivate, inactivate, [def]).
semw(associate,attach,attach,[def]).
semw(associated, attach, attach, [def]).
semw(associates, attach, attach, [def]).
semw(association, attach, attach, [def]).
semw(attach, attach, attach, [def]).
semw(attached ,attach,attach,[def]).
semw(attaches, attach, attach, [def]).
semw(attachment, attach, attach, [def]).
semw(bind, attach, attach, [def]).
semw(binding, attach, attach, [def]).
semw(binds,attach,attach,[def]).
semw(block, inactivate, inactivate, [def]).
semw(blocked, inactivate, inactivate, [def]).
semw(blocking,inactivate,inactivate,[def]).
semw(blocks,inactivate,inactivate,[def]).
semw(bound,attach, attach,[def]).
                         'break bond', [def]).
semw(break, breakbond,
semw(breakage, breakbond,
                            'break bond', [def]).
semw(breaks, breakbond,
                          'break bond', [def]).
semw(broke, breakbond,
                         'break bond', [def]).
semw(broken, breakbond, 'break bond', [def]). % case without break
bond
semw(catalyzation, promote, catalyze, [def]).
semw(catalyze,promote,catalyze,[def]).
semw(catalyzed,promote,catalyze,[def]).
semw(catalyzes,promote,catalyze,[def]).
semw(catalyzing,promote, catalyze,[def]).
semw(cause, cause, cause, [def]).
semw(caused, cause, cause, [def]).
semw(causes, cause, cause, [def]).
```

```
'break bond', [def]).
semw(cleavage, breakbond,
semw(cleave, breakbond,
                         'break bond', [def]).
semw(cleaved, breakbond,
                          'break bond', [def]).
semw(cleaves, breakbond,
                          'break bond', [def]).
semw(coimmunoprecipitate, attach, attach, [def]).
semw(coimmunoprecipitated ,attach,attach,[def]).
semw(coimmunoprecipitates, attach, attach, [def]).
semw(coimmunoprecipitation ,attach,attach,[def]).
semw(combination ,attach,attach,[def]).
semw(combine ,attach,attach,[def]).
semw(combined ,attach,attach,[def]).
semw(combines, attach, attach, [def]).
semw(conjugate ,attach,attach,[def]).
semw(conjugated ,attach,attach,[def]).
semw(conjugates, attach, attach, [def]).
semw(conjugation ,attach,attach,[def]).
semw(connect ,attach,attach,[def]).
semw(connected ,attach,attach,[def]).
semw(connection, attach, attach, [def]).
semw(connects, attach, attach, [def]).
semw(constrain, inactivate, inactivate,[def]).
semw(constrained, inactivate, inactivate, [def]).
semw(constrains, inactivate, inactivate, [def]).
semw(constraint, inactivate, inactivate, [def]).
semw(coprecipitate, attach, attach, [def]).
semw(coprecipitated, attach, attach, [def]).
semw(coprecipitates, attach, attach, [def]).
semw(coprecipitation ,attach,attach,[def]).
semw(copurification ,attach,attach,[def]).
semw(copurified ,attach,attach,[def]).
semw(copurifies, attach, attach, [def]).
semw(copurify ,attach,attach,[def]).
semw(couple ,attach,attach,[def]).
semw(coupled, attach, attach, [def]).
semw(couples, attach, attach, [def]).
semw(cut, breakbond,
                      'break bond', [def]). % leave breakbond onl
y?
semw(cuts, breakbond, 'break bond', [def]).
semw(deactivate, inactivate, inactivate, [def]).
semw(deactivated, inactivate, [def]).
semw(deactivates, inactivate, inactivate, [def]).
semw(deactivation, inactivate, inactivate, [def]).
semw(death, process, death,[1]).
```

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semw(demethylate, breakbond, demethylate, [def]).
semw(demethylated, breakbond, demethylate,[def]).
semw(demethylates, breakbond, demethylate, [def]).
semw(demethylation, breakbond, demethylate, [def]).
semw(dephosphorylate, breakbond,dephosphorylate,[def]).
semw(dephosphorylated, breakbond,dephosphorylate,[def]).
semw(dephosphorylates, breakbond,dephosphorylate,[def]).
semw(dephosphorylation, breakbond,dephosphorylate,[def]).
semw(die, process, death,[1]).
semw(died, process, death,[1]).
semw(dies, process, death,[1]).
semw(disassemble, release, release, [def]).
semw(disassembled, release, release, [def]).
semw(disassembles, release, release, [def]).
semw(disassembly, release, release, [def]).
semw(discharge, release, release, [def]).
semw(discharged, release, release, [def]).
semw(discharges, release, release, [def]).
semw(disengage, release, release, [def]).
semw(disengaged, release, release, [def]).
semw(disengagement, release, release, [def]).
semw(disengages, release, release, [def]).
semw(divide, breakbond,
                          'break bond', [def]).
                           'break bond', [def]).
semw(divided, breakbond,
semw(divides, breakbond,
                          'break bond', [def]).
semw(division, breakbond,
                           'break bond', [def]).
semw(dying, process, death,[1]).
semw(enhance,promote,promote,[def]).
semw(enhanced, promote, promote, [def]).
semw(enhancement, promote, promote, [def]).
semw(enhances, promote, promote, [def]).
semw(enhancing, promote, promote, [def]).
semw(express, generate, express, [def]). % can have either 1 or 2 ar
guments
semw(expressed, generate,express,[def]).
semw(expresses, generate, express, [def]).
semw(expressing, generate, express, [def]).
semw(expression, generate, express, [def]).
semw(generate,generate,generate,[def]).
semw(generated,generate,generate,[def]).
semw(generates, generate, generate, [def]).
semw(generating,generate,generate,[def]).
semw(generation, generate, generate, [def]).
```

```
semw(hew, breakbond,
                     'break bond',[def]).
semw(hewed, breakbond, 'break bond', [def]).
semw(hews, breakbond,
                       'break bond', [def]).
semw(hinder, inactivate, inactivate, [def]).
semw(hindered, inactivate, inactivate, [def]).
semw(hinders, inactivate, inactivate, [def]).
semw(hindrance, inactivate, inactivate, [def]).
semw(inactivate, inactivate, inactivate, [def]).
semw(inactivated, inactivate, inactivate, [def]).
semw(inactivates, inactivate, inactivate, [def]).
semw(inactivation, inactivate, inactivate, [def]).
semw(incite, activate, activate, [def]).
semw(incited, activate, activate, [def]).
semw(incitement, activate, activate, [def]).
semw(incites, activate, activate, [def]).
semw(induce, activate, activate, [def]).
semw(induced, activate, activate, [def]).
semw(induces, activate, activate, [def]).
semw(induction, activate, activate, [def]).
semw(influence, activate, activate, [def]).
semw(influenced, activate, activate, [def]).
semw(influences, activate, activate, [def]).
semw(influencing, activate, activate, [def]).
semw(inhibit, inactivate, inactivate,[def]).
semw(inhibited, inactivate, inactivate, [def]).
semw(inhibition, inactivate, inactivate, [def]).
semw(inhibits, inactivate, inactivate, [def]).
semw(initiate, activate, activate, [def]).
semw(initiated, activate, activate, [def]).
semw(initiates, activate, activate, [def]).
semw(initiattion, activate, activate, [def]).
semw(instigate, activate, activate, [def]).
semw(instigated, activate, activate, [def]).
semw(instigates, activate, activate, [def]).
semw(instigation, activate, activate, [def]).
semw(interact, interact, interact, [def]).
semw(interacted, interact, interact, [def]).
semw(interaction, interact, interact, [def]).
semw(interactions, interact, interact, [def]).
semw(interacts, react, interact,[def]).
semw(join ,attach,attach,[def]).
semw(joined ,attach, attach, [def]).
semw(joining, attach, attach, [def]).
```

```
semw(joins, attach, attach, [def]).
semw(juncture, attach, attach, [def]).
semw(liberate, release, release, [def]).
semw(liberated, release, release, [def]).
semw(liberates, release, release, [def]).
semw(liberation, release, release, [def]).
semw(limit, inactivate, inactivate, [def]).
semw(limitation, inactivate, inactivate, [def]).
semw(limited, inactivate, inactivate, [def]).
semw(limits, inactivate, inactivate, [def]).
semw(link, attach, attach, [def]).
semw(linked, attach, attach, [def]).
semw(linking, attach, attach, [def]).
semw(links,attach, attach,[def]).
semw(mediate, promote, promote, [def]).
semw(mediated, promote, promote, [def]).
semw(mediates, promote, promote, [def]).
semw(mediation, promote, promote, [def]).
semw(methylate, createbond, methylate,[def]).
semw(methylated, createbond, methylate,[def]).
semw(methylates, createbond, methylate,[def]).
semw(methylation, createbond, methylate,[def]).
semw(modification, modify, modify, [def]).
semw (modified, modify, modify, [def]).
semw (modifies, modify, modify, [def]).
semw(modify, modify, modify, [def]).
semw (modifying, modify, modify, [def]).
semw(mutate, modify, mutate, [1]).
semw(mutated, modify, mutate, [1]).
semw(mutates, modify, mutate, [1]).
semw(mutating, modify, mutate, [1]).
semw(mutation, modify, mutate, [1]).
semw(overexpressed, generate,overexpress,[def]).
semw(overexpresses, generate,overexpress,[def]).
semw(overexpressing, generate, overexpress, [def]).
semw(overexpress, generate, express, [def]).
semw(overexpression,generate,overexpress,[def]).
semw(pair, attach, attach, [def]).
semw(paired, attach, attach, [def]).
semw(pairing, attach, attach, [def]).
                    attach, [def]).
semw (pairs, attach,
semw(phosphorylate, createbond, phosphorylate,[def]).
semw(phosphorylated, createbond, phosphorylate, [def]).
```

```
semw(phosphorylates, createbond, phosphorylate,[def]).
semw(phosphorylation, createbond, phosphorylate,[def]).
semw(precede, cause, cause, [def]).
semw(preceded, cause, cause, [def]).
semw(precedes, cause, cause, [def]).
semw(preceding, cause, cause, [def]).
semw(promote, promote, [def]).
semw(promoted, promote, [def]).
semw(promotes, promote, promote, [def]).
semw(promotion, promote, promote, [def]).
semw(prompt, activate, activate, [def]).
semw(prompted, activate, activate, [def]).
semw(prompting, activate, activate, [def]).
semw(prompts, activate, activate, [def]).
semw(react, react, [def]).
semw(reacted, react, react, [def]).
semw(reaction, react, react, [def]).
semw(reactions, react, react, [def]).
semw(reacts, react, [def]).
semw(regulate, signal, signal, [def]).
semw(regulated, signal, signal, [def]).
                                             % B is regulated by
   A --> B
semw(regulates, signal, signal, [def]).
semw(regulation, signal, signal, [def]).
semw(release, release, release, [def]).
semw(released, release, release, [def]).
semw(releases, release, release, [def]).
semw(removal, breakbond, 'break bond ',[def]).
semw(remove, breakbond, 'break bond ',[def]).
semw(remove, breakbond, 'break bond ', [def]).
semw(removes, breakbond, 'break bond ', [def]).
semw(replace, substitute, substitute, [def]).
semw(replaced,
                substitute, substitute, [def]).
semw(replacement, substitute, substitute, [def]).
semw(replaces, substitute, substitute,[def]).
semw(repress, inactivate, inactivate, [def]).
semw(repressed, inactivate, inactivate, [def]).
semw(represses, inactivate, inactivate, [def]).
semw(repression, inactivate, inactivate, [def]).
semw(require, cause, cause, [2, rev]).
semw(required, cause, cause, [2, rev] ).
semw(requirement, cause, cause, [2, rev]).
semw(requires, cause, cause, [2, rev] ).
```

```
semw(requiring, cause, cause, [2, rev] ).
semw(restrain, inactivate, inactivate, [def]).
semw(restrained, inactivate, inactivate, [def]).
semw(restrains, inactivate, inactivate, [def]).
semw(restraint, inactivate, inactivate, [def]).
semw(sensitization, activate, activate, [def]).
semw(sensitize, activate, activate, [def]).
semw(sensitized, activate, activate, [def]).
semw(sensitizes, activate, activate, [def]).
semw(separate, breakbond, 'break bond', [def]).
semw(separated, breakbond, 'break bond', [def]).
semw(separates, breakbond,
                            'break bond', [def]).
semw(separation, breakbond,
                             'break bond', [def]).
semw(sever, breakbond,
                        'break bond', [def]).
semw(severance, breakbond,
                            'break bond', [def]).
semw(severed, breakbond,
                           'break bond', [def]).
semw(severs, breakbond,
                         'break bond', [def]).
semw(signal, signal, [def]).
semw(signaled, signal, signal, [def]).
semw(signaling, signal, signal, [def]).
semw(signals, signal, signal, [def]).
semw(split, breakbond, 'break bond',[def]).
semw(splits, breakbond,
                        'break bond', [def]).
semw(splitting, breakbond, 'break bond', [def]).
semw(stimulate, activate, activate, [def]).
semw(stimulated, activate, activate, [def]).
semw(stimulates, activate, activate, [def]).
semw(stimulation, activate, activate, [def]).
semw(substitute, substitute, [def]).
semw(substituted, substitute, substitute, [def]).
semw(substitutes, substitute, substitute, [def]).
semw(substitution, substitute, substitute, [def]).
semw(suppress, inactivate, inactivate, [def]).
semw(suppressed, inactivate, inactivate, [def]).
semw(suppresses, inactivate, inactivate,[def]).
semw(suppression, inactivate, inactivate, [def]).
semw(tie,attach,attach,[def]).
semw(tied, attach, attach, [def]).
semw(ties, attach, attach, [def]).
semw(transcribe,generate,transcribe,[def]).
semw(transcribed,generate,transcribe,[def]).
semw(transcribes,generate,transcribe,[def]).
semw(transcribing,generate,transcribe,[def]).
```

```
semw(transcription, generate, transcribe, [def]).
semw(ubiquitinize, createbond, ubiquitinize, [def]).
semw(ubiquitinize, createbond, ubiquitinize,[def]).
semw(ubiquitinized, createbond, ubiquitinize,[def]).
semw(ubiquitinizes, createbond, ubiquitinize, [def]).
semw(urge, activate, activate, [def]).
semw(urge, activate, activate, [def]).
semw(urged, activate, activate, [def]).
semw(urges, activate, activate, [def]).
semw(urging, activate, activate, [def]).
semw(form, attach, attach, [def]).
semw(forms, attach, attach, [def]).
semw(formed, attach, attach, [def]).
semw(forming, attach, attach, [def]).
semw(formation, attach, attach, [def]).
semw(assemble, attach, attach, [def]).
semw(assembles, attach, attach, [def]).
semw(assembled, attach, attach, [def]).
semw(assembling, attach, attach, [def]).
semw(assembly,attach,attach,[def]).
semw(dissassemble, release, release, [def]).
semw(dissassembles, release, release, [def]).
semw(dissassembled, release, release, [def]).
semw(dissassembling, release, release, [def]).
semw(dissassembly, release, release, [def]).
semw(dissociate, release, release, [def]).
semw(dissociates, release, release, [def]).
semw(dissociated, release, release, [def]).
semw(dissociating, release, release, [def]).
semw(dissociation, release, release, [def]).
semw(recruit,attach,attach,[def]).
semw(recruits,attach,attach,[def]).
semw (recruited, attach, attach, [def]) ...
semw(recruiting,attach,attach,[def]).
semw(recruitment, attach, attach, [def]).
```

```
% edited Genome grammar - adapted from MedLEE's grammar for use with MedLEE
* this is to be used along with the genomics lexicon of substances, actions,
   and relations.
% revised March 16, April 5, 2000
% adjusted for tagged input
:- multifile(wdef/3).
:- multifile(phrase/5).
Written by Carol Friedman for the MedLEE System
ş.
*
     Queens College of the City University of New York
                                                                      %
% Highest Level Predicate - sem_sent - 1st arg. is target structure

    2nd arg. is a list of words in sentence%

                                 - 3rd arg. is '[]'
* Target structure: a frame or set of connected frames:
         the frame describes an action or several related actions;
         an action frame is a list consisting of the symbol 'action'
         followed by the code for the action and arguments.
         The arguments are either substances or actions;
         each substance slot consists of the name of the type of
         substance followed by the value for the substance;
         the substance slot may contain slots for several substances.
% Examples:
% Blocking of i1-2 gene transcription by activated rap1.
% (action, inactivate, [protein, Rap1, [state, active]],
                   [action, transcribe, [x], [gene, interleukin-2]]]
* The adapter protein crkl was associated with both phosphorylated cbl and the*
% guanidine nucleotide-releasing factor c3g.
% (action,attach,[protein,CrkL],
               [relation, and, [protein, Cbl, [state, phosphorylated]],
                          [protein, guanidine nucleotide-releasing factor C3G,
                                               fail an unknown predicate
:- unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=,~=]). % same priority and type as = or ==
% snoop is generally used to find input string when using a DCG
       the input string is used for constraints
snoop (A, B, A, B).
sem_sent(P,Semlist,X) -->
       {assert(addstotal(0))},
       sem parse (P, Semlist, X).
sem_parse(Target,Semlist) -->
       sem_patterns(P,Semlist).
sem_parse(Target, Semlist, X) -->
       sem_patterns(P,Semlist),
       sem_endornot(P,Target,X).
sem_parse([failure],_,X,_,_) :-
       addstotal(X).
sem_endornot(P,P,X) --> % P is target if there is an endmark
```

Appendix D

```
sem endmark,
        {addstotal(X)}. % X is number of times reached endmark
sem_endornot(_,_,_,_,_)
                      :- % did not reach endmark; update count and fail
       uptotal, fail.
sem_endornot(_,[failure],X,_,_) :-
       addstotal(X), % X is number of times reached
% Finding patterns
sem_patterns(F,Semlist) -->
       pattern(F1, Semlist),
       morepattern(R,F2,Semlist), % connected patterns
       {getrelation(R,F1,F2,F)}.
/**************************
* The action pattern types are: pattern, nounactionpatt, actpatt, and *
* nounactpatt.
* pattern --> actionarg(A1)
             active or passive verb
             actionarg(A2).
* pattern --> nounactionpatt.
* pattern --> actpatt.
_
********************
% pattern is saved in a symbol table (st); check for success/failure 1st
% Case where pattern is in st and has been successful
pattern(Fmt,_) --> checkst(pattern, ,s,Fmt).
% Case where pattern is in st as a failure.
pattern(_,_) --> checkst(pattern, ,f, ), {!, fail}.
$ pattern 5: an action pattern with a nominal verb
% Ps1 cleavage by zvad.
% apoptosis-induced cleavage of PS2 by zDEVD.
pattern(F, Semlist) -->
    snoop(S0,S0),
   { \+ checkst(pattern, 5, _, _, S0, _),
    actionchk(Semlist) },
    nounactionpatt(F),
    snoop(S,S),
   { addst(pattern, 5, s, F, S0, S)
  }.
% pattern 1: an action/substance acts on an action/substance
the activation of rap1 inhibits the expression of il-2
* rapl functions as a negative regulator of tcr-mediated il-2 gene
transcription.
pattern(F,Semlist) -->
                       snoop(S0,S0), % S0 is the input string
   { \+ checkst(pattern,1,_,_,S0,_),
    actionchk(Semlist),
    connectchk(Semlist) },
    actionarg(A1),
```

```
connectact (Sem, [v, vp, ved], Target, Features),
     actionarg(A2),
     snoop(S,S), %ending sentence list
   { member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst(pattern, 1, s, F, SO, S)
   }.
% pattern 2: an action/substance was acted on by an action/substance
* The aggregation of bad was suppressed.
% The aggregation of bad was suppressed by the phosphorylation of jnk.
% Grb2 was associated with Cbl.
% Apoptosis-associated cleavage of endogenous PS1 was blocked by the
% treatment with zVAD.
pattern(F,Semlist) -->
     snoop(S0,S0), % S0 is the input string
    { \+ checkst(pattern, 2, _, _, S0, _),
      actionchk (Semlist),
      connectchk(Semlist) },
      actionarg(A2),
      sem beterm(),
                       % was
      connectact (Sem, [ven], Target, Features), %activated
      optbyarg(A1),
      snoop(S,S), %ending sentence list
   { (member(def, Features),
      modlist([A1,A2,Site],Mods);
      member (rev, Features),
      modlist([A2,A1,Site],Mods)),
      frame (F, action, Target, Mods),
      addst(pattern, 2, s, F, S0, S)
   }.
% pattern 3: an action/substance acted on an action/substance
% bad induced phosphorylation of fyn.
% tcr and cd28-mediated il-2 transcription.
pattern(F, Semlist) -->
     snoop(S0,S0),
   { \+ checkst(pattern, 3, _, _, S0, _),
     actionchk (Semlist),
     connectchk(Semlist) },
     actionarg(A1), % substance or basic action
   % optdash,
     % optof,
     actionarg(A2), % had pattern here
     snoop(S,S),
  { (member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst(pattern, 3, s, F, S0, S)
  }
```

```
$ pattern 4: a simple action pattern with an active verb.
% Activated Raf-1 phosphorylates MEK-1.
pattern(F,Semlist) -->
     snoop(S0,S0),
     %check that sentence has an action word/phrase
   { \+ checkst(pattern, 4,_,_,S0,_),
     actionchk(Semlist) },
     actpatt(F),
     snoop(S,S),
   { addst(pattern, 4, s, F, S0, S)
  }.
% no more patterns - save failure
pattern(_,_) --> addst(pattern,0,f,_), {!, fail}.
$ sem morepattern(-Rel,-P,+Semlist,+S0,+S):
*
        Rel is a relation and its value frame;
        P is the remaining patterns, Semlist is the list of semantic classes
*
        in sentence
% if have a series of ','s, use the relation "and" or "or" if in the nest
% and make that the relation
morepattern(R,F,Semlist) -->
        sem relation(R1, Mod1),
                                 *relation and modifiers
        sem patterns(F, Semlist),
        {(frame(F,rel,Conj2,_), % F contains nested relation
            (Conj2 = and; Conj2 = or), frame(R1,rel,',',_), % R1 relation frame
           frame(R,rel,Conj2, ) % value of relation is Conj2
           R1 = [], % where do Type, Value and Mods2 come from?
          frame(R1, Type, Value, Mod2), % get components of original relation
          mergemods (Mod1, Mod2, Mods),
          ( Mods = [], frame(R, rel, Value, []), !;
            %frame(R,rel,[Value|Mods],[]) % make it rel connector with rel mod
            R = [rel, [Value | Mods]]
          )
         ).
        }.
% no more findings
morepattern([],[], ,S,S).
% actionarg is the argument of pattern
% actionarg is either a substance or a basic action
% actionarg is saved in a symbol table (st); check for success/failure 1st
% Case where actionarg is in st and have been successful
actionarg(A) --> checkst(actionarg,_,s,A).
% Case where actionarg is in st as a failure.
actionarg(_) --> checkst(actionarg,_,f;_), {!, fail}.
% actionarg 1: a substance or substances
% Rap1, active Rap1, Cbl and Crkl
actionarg(A) --> snoop(S0,S0), % S0 is the input string
              { \+ checkst(actionarg,1,_,_,S0,_)},
                substances (A),
                snoop(S,S),
              { addst(actionarg,1,s,A,S0,S) }.
```

```
% actionarg 2: a process like apoptosis, or a disease
actionarg(A) --> snoop(S0,S0), % S0 is the input string
               { \+ checkst(actionarg, 2, _, _, 50, _) },
                processpatt(A),
                snoop(S,S),
               { addst(actionarg, 2, s, A, S0, S)
   }.
% actionarg 3: a nominal action pattern
% Etoposide-induced apoptosis.
% Etoposide-induced PS1 cleavage by 2VAD.
actionarg(A) --> snoop(S0,S0), % S0 is the input string
              { \+ checkst(actionarg, 3, _, _, S0, _) },
                nounactionpatt(A),
                snoop(S,S),
                 {addst(actionarg, 3, s, A, S0, S)
   } .
% actionarg 4: the object of the nominal action is an actionarg
% Blocking of IL-2 Gene transcription by activated rapl.
actionarg(A) --> snoop(S0,S0), % S0 is the input string
                 { \+ checkst(actionarg, 4 , _ , _ , S0, _) },
                   action (Sem, [n, ving], Target, Features),
                    [of],
                   actionarg(Al),
                   optbyagent (A2),
                    snoop(S,S),
                 { (member(def, Features),
                   modlist([A1,A2],Mods);
                   member (rev, Features),
                   modlist([A2,A1],Mods)),
                    frame (A, action, Target, Mods),
                    addst(actionarg, 4, s, A, S0, S)
     }.
no more actionarg - save failure ·
actionarg(_) --> addst(actionarg,0,f,_), {!, fail}.
* nounactionpatt is a nominal action pattern which allows for left and right
11-2 gene transcription mediated by tcr and cd28 was inhibited by rap1.
* Activated rap1 functions as a negative regulator of tcr and cd-28-mediated
il 2 transcription.
f nounactionpatt is saved in a symbol table (st); check for success/failure 1st
t Case where nounactionpatt is in st and has been successful
nounactionpatt(A) --> checkst(nounactionpatt,_,s,A).
Case where nounaction patt is in st as a failure.
nounactionpatt(_) --> checkst(nounactionpatt,_,f,_), {!, fail}.
nounactionpatt(P) --> snoop(S0,S0),
                                       % SO is the input string
                     { \+ checkst(nounactionpatt,1,_,_,S0,_)},
                      actionlmod(L, Syn1),
                      nounactionunit(A),
                      actionrmod(R, Syn2),
```

```
snoop(S,S),
                     { (Syn1 = ved, append(R, [A], RA),
                       append(L, RA, P);
                        Syn1 = ving, append(R, [A], RA),
                       L = [action, Verb, Object],
                       modlist(RA, Object, Mods),
                        frame (P, action, Verb, Mods)),
                       addst(nounactionpatt,1,s,P,S0,S) }.
% no more nounactionpatt - save failure
nounactionpatt(_) --> addst(nounactionpatt,0,f,_), {!, fail}.
% the central unit of the nounactionpatt is a nounactpatt or a process
nounactionunit(A) --> nounactpatt(A).
nounactionunit(A) --> process(A).
% left modifiers of nounactpatt
% Zvad-inhibited cleavage pf Ps1
actionlmod(L, ved) --> substances(S),
                      optdash,
                       action(Sem, [ved], Target, Features),
                     { frame(L, action, Target, [S]) }.
% apoptosis induced cleavage of ps2
actionlmod(L, ved) --> process(S),
                      optdash,
                       action(Sem, [ved], Target, Features),
                     { frame(L, action, Target, [S]) }.
% apoptosis causing cleavage of Ps1 by Zvad.
% need to invert the order of nounactpatt and action1mod
actionlmod(L, ving) --> processobject(A), % process or nounacpatt,
                        action (Sem, [ving], Target, Features),
                      { frame(L,action, Target,A) }.
actionlmod([],_) --> [].
actionrmod(R, ved) --> action(Sem, [ved], Target, Features),
                      byagent(A), % may have to add ving to actionrmod
                    { frame(R,action, Sem, A) }.
actionrmod([],_) --> [].
% actpatt parses a simple action between substances expressed by an active verb
* actpatt is saved in a symbol table (st); check for success/failure * * 1st
% Case where actpatt is in st and has been successful
actpatt(F) --> checkst(actpatt,_,s,F).
% Case where actpatt is in st as a failure.
actpatt(_) --> checkst(actpatt,_,f,_), {!, fail}.
% actpatt 1: substance acts on substance
% PDK1 phosphorylates p70s6k at Thr229
actpatt(F) -->
    snoop(S0,S0), % S0 is the input string
  { \+ checkst(actpatt,1 ,_,_,S0,_)},
```

```
substances (A1),
    sem whichrel,
                      % opt 'that'
    action (Semclass, [vp, ved], Target, Features),
    prepopt. % added prepopt to allow action 'to' and 'with' substance
    substances (A2),
    siteinfo(Site),
    snoop(S,S),
  { (member(def, Features),
    modlist([A1,A2,Site],Mods);
    member (rev, Features),
    modlist([A2,A1,Site],Mods)),
    frame(F,action,Target,Mods),
    addst(actpatt,1 ,s,F,S0,S)
% acpatt 2:
% Substance was bound by Substance
% Substance was associated to substance.
% F can give either first or second place to the second argument;
% a byagent gets first position; prepagent gets second.
% Phosphorylated Fyn was associated with Cbl.
actpatt(F) -->
    snoop(S0,S0), % S0 is the input string
 { \+ checkst(actpatt, 2, _, _, S0, _) }.
    substances (A1),
    sem beterm(),
    action (Semclass, [ven], Target, Features),
    optbyorprepagent (Position, A2),
    snoop(S,S),
 { (member(def, Features),
   (Position=second, modlist([A1,A2,Site],Mods);
    Position = first, modlist([A2,A1,Site],Mods));
    member (rev, Features),
   (Position=second, modlist([A2,A1,Site],Mods);
    Position= first, modlist([A1,A2,Site],Mods))),
    frame (F, action, Target, Mods),
    addst(actpatt, 2, s, F, S0, S)
 }.
% no more actpatt - save failure
actpatt(_) --> addst(actpatt,0,f,_), {!, fail}.
% nounactpatt parses a simple action between substances expressed by a nominal
% verb
% nounactpatt is saved in a symbol table (st); check for success/failure 1st
% Case where nounactpatt is in st and have been successful
nounactpatt(Fmt) --> checkst(nounactpatt,_,s,Fmt).
% Case where nounactpatt is in st as a failure.
nounactpatt(_) --> checkst(nounactpatt,_,f,_), {!, fail}.
% nounactpatt 1:
% Jnk phosphorylation of Bad
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
```

```
{ \+ checkst(nounactpatt,1,_,_,S0,_) },
    substances(A1),
    {aminoacidtest(A1)},
    optdash,
    action (Semclass, [n], Target, Features),
    ofobject (A2),
    siteinfo(Site),
    snoop(S,S),
   { (member (def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst(nounactpatt, 1, s, F, S0, S)
   }.
% nounactpatt 2: the binding of substance and substance
* association of Fyn and Cbl.
% the reason for having this as a separate pattern is to
% prevent 'Fyn and Cbl' from being parsed together as substances
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
   \+ checkst(nounactpatt,2 ,_,_,S0,_) },
    action(attach, [ving, n], Target, Features),
    ofobject1(A1),
    andobject(A2),
 $ siteinfo(Site),
    snoop(S,S),
 { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Mods),
    addst(nounactpatt,2,s,F,S0,S)
* nounactpatt 3:
* The cleavage of protein by substance.
* Association of phosphorylated Fyn with Cbl
* Tyrosine phosphorylation of Cbl by kinase
optbyorprepagent determines the order of arguments; byagent is placed first;
prepagent is placed second
nounactpatt(F) -->
   snoop(S0,S0), % S0 is the input string
    { \+ checkst(nounactpatt,3 ,_,,_,S0,_)},
    actionof(F),
    snoop(S,S),
  { addst(nounactpatt,3 ,s,F,S0,S) }.
actionof(F) -->
    siteinfo(Site),
    action(Semclass, [ving, n], Target, Features),
    optofobject (A1),
    optbyorprepagent (Position, A2),
    snoop(S,S),
  { (member(def, Features),
     (Position=second, modlist([A1,A2,Site],Mods);
     Position= first, modlist([A2,A1,Site],Mods));
     member (rev, Features),
```

```
(Position=second, modlist([A2,A1,Site],Mods);
     Position= first, modlist([Al,A2,Site],Mods))),
     frame (F, action, Target, Mods)
  }.
% nounactpatt 4:
% Fyn association with Cbl.
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
  { \+ checkst(nounactpatt, 4, _, _, S0, _) },
    substances (A1),
    action(Semclass, [ving, n], Target, Features),
    withobject (A2),
  % siteinfo(Site),
    snoop(S,S),
    modlist([A1, A2, Site], Mods),
    frame (F, action, Target, Mods),
    addst (nounactpatt, 4, s, F, S0, S)
 }.
aminoacidtest(X) :- X \= [aminoacid | ].
% nounactpatt 5:
% IL-2 gene transcription
% Cbl phosphorylation [by substance or action]
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
    \+ checkst(nounactpatt,5 ,_,_,S0,_) },
    substances (A2),
    optdash,
    action(Semclass, [n], Target, Features),
    optbyagent (A1),
 % siteinfo(Site),
    snoop(S,S),
 { (member(def, Features),
    modlist([A1,A2,Site],Mods);
    member (rev, Features),
    modlist([A2,A1,Site],Mods)),
    frame (F, action, Target, Mods),
    addst(nounactpatt, 5 , s, F, S0, S)
 }.
% nounactpatt 6:
% fyn-cbl association.
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
    \+ checkst(nounactpatt,6 , , ,S0, ) },
   substances(Al),
    optdash,
    substances (A2),
    action(Semclass, [n, ving], Target, Features),
 % siteinfo(Site),
    snoop(S,S),
  { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Mods),
    addst (nounactpatt, 6, s, F, S0, S)
  }.
```

```
% nounactpatt 7:
% Cbl phosphorylated by fyn.
nounactpatt(F) -->
    snoop(SO,SO), % SO is the input string
    { \+ checkst(nounactpatt,7,_,_,S0,_)},
    substances (A1),
    action(Semclass, [ven], Target, Features),
    (by),
    substances (A2),
 % siteinfo(Site),
    snoop(S,S),
             { (member(def, Features),
    { modlist([A2,A1,Site],Mods),
             member (rev, Features),
             modlist([A1,A2,Site],Mods)),
      frame (F, action, Target, Mods),
      addst(nounactpatt,7,s,F,S0,S)
    }.
% no more nounactpatt - save failure
nounactpatt(_) --> addst(nounactpatt,0,f,_), {!, fail}.
connectact(Sem, Syn, Target, Features) -->
      action (Sem, Syn, Target, Features),
     {member(Sem, [cause, cause1, activate, inactivate, signal, substitute, promote])}.
connectacts (Sem, Syn, Target, Features) -->
      connectact (Sem, Syn, Target, Features).
% aminoacid like tyrosine : ex.: tyrosine Cbl phosphorylation
% at position 201 Thr
siteinfo(S) --> aminoacid(A),
                  {frame(S, site, [A], [])} .
siteinfo(S)
                 sitepreps, % 'in', 'at'
                position(S).
siteinfo([]) --> [].
              --> prepterm(in,_).
sitepreps
              --> prepterm(at,_).
sitepreps
position(S)
             --> [position],
                  sem_integerterm(I),
                { frame(S, site, I, []) }.
The definitions of actions refer to the lexicons lexsynact.pl and lexsemact.pl
$ Sem is the semantic class; Syn is the syntactic class
% F is the target
% oneaction was added for use with moreaction to allow parsing of conjoined
% actions
oneaction(activate, Syn, F, Features)
                                       --> activateterm(Syn, F, Features), {!}.
oneaction(attach, Syn, F, Features)
                                       --> attachterm(Syn, F, Features), {!}.
oneaction(breakbond, Syn, F, Features)
                                       --> breakbondterm(Syn,F,Features),{!}.
```

```
--> createbondterm(Syn, F, Features), {!}.
oneaction(createbond, Syn, F, Features)
                                        --> inactivateterm(Syn, F, Features), {!}.
oneaction(inactivate, Syn, F, Features)
oneaction(react, Syn, F, Features)
                                         --> reactterm(Syn, F, Features), {!}.
oneaction(release, Syn, F, Features)
                                         --> releaseterm(Syn, F, Features), {!}.
oneaction(signal, Syn, F, Features)
                                         --> signalterm(Syn, F, Features), {!}.
                                         --> substituteterm(Syn, F, Features), {!}.
oneaction(substitute, Syn, F, Features)
                                         --> transcribeterm(Syn, F, Features), {!}.
oneaction(transcribe, Syn, F, Features)
                                         --> promoteterm(Syn, F, Features), (!).
oneaction(promote, Syn, F, Features)
                                         --> generateterm(Syn, F, Features), {!}.
oneaction (generate, Syn, F, Features)
                                             causeterm(Syn, F, Features), {!}.
oneaction(cause, Syn, F, Features)
                                      --> activateterm(Syn, A1, Features),
action(activate, Syn, F, Features)
                             moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
                                     --> attachterm(Syn,A1 ,Features),
action(attach, Syn, F, Features)
                            moreaction(Conj, Args),
                            {Conj = [],F =A1;
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]).
                                     --> breakbondterm(Syn, F, Features),
action(breakbond, Syn, F, Features)
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action, Al]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(createbond, Syn, F, Features) --> createbondterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = Al;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
action(inactivate,Syn,F,Features) --> inactivateterm(Syn,F,Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = Al;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1].
action(react, Syn, F, Features)
                                     --> reactterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]}.
                                      --> releaseterm(Syn,F,Features),
action(release, Syn, F, Features)
                            moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[]; mergemods([[action, A1]], Args, Actions);
                            frame(F1, relation, Conj, Actions), F = [F1] }.
action(signal,Syn,F,Features)
                                    ---> signalterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
action(substitute,Syn,F,Features) --> substituteterm(Syn,F,Features),
                            moreaction (Conj, Args),
                            \{Conj = [], F = A1;
                            Conj = [], mergemods ([[action, A1]], Args, Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]).
action(transcribe,Syn,F,Features) --> transcribeterm(Syn,F,Features),
```

```
moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F = {F1}}.
action(promote, Syn, F, Features)
                                     --> promoteterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action, A1]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(generate, Syn, F, Features)
                                     --> generateterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
action(cause, Syn, F, Features)
                                  --> causeterm(Syn,F,Features),
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
% binds, phosphorylates and activates
moreaction(Conj, Args) --> sem conjrest(Conj1),
                            oneaction (Sem, Syn, A, Features),
                            moreaction(Conj2, Alist),
                           {Conj2 = [], Alist=[], Conj=Conj1, Args = [[action, A]];
                            Conj2 = [], Conj = Conj2,
                            addmod([action,A],Alist,Args) }.
moreaction([],[],S,S).
passiveconnect(Sem, [ven], Target, Features) -->
                  sem beterm(),
                  connectact (Sem, [ven], Target, Features).
processpatt(A) --> disease(A).
processpatt(A) --> process(A).
optbyorprepagent(first,A) --> byagent(A).
optbyorprepagent(second, A) --> prepagent(A).
optbyorprepagent(first,A) \longrightarrow [], \{A = x\}.
byorprepagent(first,A) --> byagent(A).
byorprepagent (second, A) --> prepagent (A).
optbyagent(A) --> byagent(A).
optbyagent(A) --> [], {A = [x]}.
byagent(A) --> [by],
               substances (A).
byagent(A) --> [by],
                nounactionpatt(A).
prepagent(A) --> withobject(A).
prepagent(A) --> toobject(A).
% prepagent(A) --> andobject(A).
prepagent(A) --> ofobject(A).
```

```
% optprepagent(A) --> byagent(A).
optprepagent(A) --> ofobject(A).
optprepagent(A) --> withobject(A).
optprepagent(A) --> toobject(A).
optprepagent(A) --> andobject(A).
optprepagent(A) --> [], {A= [x]}.
ofobject(A) --> [of],
                nounactionpatt(A).
ofobject(A) --> [of],
                substances(A).
ofobject(A) --> [of],
                actionof(A).
ofobject1(A) --> [of], substance(A). % to parse Binding of Fyn and Bad.
optofobject(A) --> ofobject(A).
optofobject([x]).--> [].
processobject(A) --> process(A). * can be expanded to nounactpatt, etc.
% optwithobject(A) --> withobject(A).
 * optwithobject(A) \longrightarrow [], {A = [x]}. 
withobject(A) --> [with], substances(A).
toobject(A) --> [to], substances(A).
andobject(A) --> [and], substances(A).
prepobject(A) --> [to], substances(A).
prepobject(A) --> [with], substances(A).
optbyarg(A) --> [by],
             actionarg(A).
optbyarg(A) --> substances(A).
optbyarg(A) --> [], {A = ['substance unknown']}.
prepopt --> [to].
prepopt --> [with].
prepopt --> [by].
prepopt --> [of].
prepopt --> [].
% toopt
toopt --> [to].
toopt --> [].
% withopt
withopt --> [with].
withopt --> [].
optdash
            --> ['-'].
optdash
            --> [ ] .
optof
optof
             --> [of].
            --> [].
/* optactionarg(A) --> actionarg(A).
optactionarg([]) --> []. */
optactionarg(A) -->
      actionarg(A).
```

```
there is no further argument
optactionarg(A) -->
    [],
    {A = []}.
% substances(F) --> substance(F).
% substances(F) --> substance(P1),
              moresubstances(Conj, Plist),
               \{ Conj = [], Plist = [], F = P1; 
욯
욯.
               Conj \= [],
             mergemods (P1, Plist, Args),
¥
                 frame (F, relation, Conj, Args)
% substances(F) --> substanceswithmods(F).
% substances(A) -->
                  proteins (A).
% subswithmods.txt
% substances is saved in a symbol table (st);
% check for success/failure 1st
t Case where substances is in st and has been successful
substances(Fmt) --> checkst(substances, ,s,Fmt).
% Case where substance is in st as a failure.
substances() --> checkst(substances,_,f,_), {!, fail}.
substances(F) -->
        snoop(S0,S0),
      { \+ checkst(substances,1,s,_,S0,_)},
        lmods(Lmods), % left modifiers
        (several substances ([relation, Conj, First | Rest]), % conjoined substances
                          % right modifiers
        rmods(Rmods),
% create list of lists containing distributed mods. of substances
      { distributesubs(Dist, [First|Rest], Lmods, Rmods),
% check Lmods - "no" F1 or F2 should be changed to no F1 and no F2
        fixconj(Lmods,[rel,Conj],[rel,C2]),
       %splice([Conj,Dist],F)
        frame(F, relation, C2, Dist);
% substances and modifiers without conjunction
        substance (D1),
        rmods(Rmods),
{D1 = [Type1, Substance1|ModsD1],
        delete(ModsD1, [], ModsD2),
        append([Lmods, Rmods], ModsD2, Allmods1),
        delete(Allmods1, [], Allmods2),
        frame(F, Type1, Substance1, Allmods2) }) ,
        snoop(S,S),
       {addst(substances, 1, s, F, S0, S)}.
/* substances(F) --> snoop(S0,S0),
                  {\+ checkst(substances, 3 , s, _, S0, _)},
                   complex(F),
                  {addst(substances, 3, s, F, S0, S)}.
% no more substances- save failure
substances(_) --> addst(substances,0,f,_), {!, fail}.
```

```
severalsubstances(F) --> substance(P1),
                         moresubstances (Conj, Plist),
                      { Conj = [], Plist = [], F = Pl;
                         Conj \= [],
                         addmod(P1, Plist, Args),
                         frame(F, relation, Conj, Args)
% ' X, Y, and Z'
 moresubstances(Conj, Args) --> sem conjrest(Conj1),
                           substance(P1),
                           moresubstances(Conj2, Plist),
                        { Conj2 = [], Plist = [], Conj = Conj1, Args = [P1];
                           Conj2 = [], Conj2 = /, Conj = Conj2,
                           addmod(P1,Plist,Args)
to allow for substances with modifiers
moresubstances(Conjl, Args) --> sem_conjrest(Conjl),
                               substances (Args), {!}.
moresubstances([],[]) --> []. % no conjunction
% distributesubs
% distributes left mods and right mods over list of findings creating
% list of lists of findings with mods
distributesubs([],[],_,_) :- !.
distributesubs(Dist,[D1|Tail],Lmods,Rmods) :-
        distributesubs(Dist2, Tail, Lmods, Rmods), %distributed for remainder
        D1 = [Type1, Substance1 [ModsD1],
        append([Lmods, Rmods], ModsD1, Allmods1),
        delete(Allmods1,[],Allmods2),
        frame (D, Type1, Substance1, Allmods2),
        append([D], Dist2, Dist). % Combine findings to get list of findings
lmods(A) --> stateterm(F),
           {frame(A, state, F, [])}.
lmods([]) --> sem_measure(_).
lmods([]) --> [].
rmods([]) --> [].
stateterm(F) --> acclex(state, F).
% for past participle of createbond and breakbond actions, the target
% is the word. ex.: phosphorylated, dephosphorylated, methylated
stateterm(F) -->
            snoop(S0,S0), % get the initial string
            createbondterm([ven], _,_),
            {SO = [F|_]}. *get the first word of the string
stateterm(F) -->
            snoop($0,50), % get the initial string
            breakbondterm([ven], _,_),
            {SO = [F]]}. *get the first word of the string
% may have to add attachterm for 'bound'
```

```
% Taken from MedLEE grammar to handle '3 cm'
sem measure(M) -->
                   sem premeasure,
                   sem_quantityterm(N),
                   optdash,
                   sem_measureterm(Unit),
                 { frame(M, measure, [N, Unit], []) }.
% complex predicates added November 8, 1999
% CrkL-C3G complex
% ras: raf-1 association
% ras: raf-1 complexes
% shc-grb2-sos
% TCR/CD3 complex
% p/CAF-p/CIP-CBP/p300-SRC-1 complex
% Ras:Raf-1 complexes
                  proteins(P),
complex(C) -->
                  {P = [A,B[],A = [], B = []},
                   optcomplexword,
                 { frame(C, complex, [P], []) }.
% a complex of NFAT4 with calcineurin
complex(C)
                 complexword,
            -->
                   complexarg(A),
                   {frame(C, complex, [A], []) }.
complexarg(A) --> [of], proteins(A).
complexarg(A) --> [between], proteins(A).
% a complex between MyD88, IRAK-2, and the IL-1Rs
complexarg(A) --> action(contain), proteins(A).
% Complexes containing BOB.1/OBF.1 and Oct proteins
proteins(P)
            --> protein(A),
                 moreproteins (P1),
                 { (A\=[]; append([A],P1,P)) }.
moreproteins(A) --> proteinconnector,
                    proteins(A).
moreproteins([]) --> [].
proteinconnector --> ['-'].
                      ['/'].
proteinconnector -->
proteinconnector -->
                       [':'].
% connector -->
                  [','].
                            taken out not to conflict with relation in
                                                               moresubstances
% connector -->
                    [and].
proteinconnector(C) --> [with].
                    proteinconnector.
optconnector -->
optconnector -->
                    [].
complexword --> [complex].
complexword --> [complexes].
complexword -->
                  ['signaling complexes'].
optcomplexword
                   --> complexword.
optcomplexword
                   --> [].
substance(A) --> protein(A).
```

```
substance(A) --> cell(A).
substance(A) --> species(A).
substance(A) --> structure(A).
substance(A) --> domain(A).
substance(A) --> gene(A).
substance(A) --> geneorprotein(A).
substance(A) --> aminoacid(A).
substance(A) --> smallmolecule(A).
substance(A) --> matter(A).
substance(A) --> proteinsite(A).
substance(A) --> disease(A).
                                        this will be modified later
substance(A) --> complex(A).
protein(A) -->
    proteinterm(P),
    {frame(A, protein, P, [])}.
complex(A) -->
    complexterm(P),
    {frame(A, complex, P, [])}.
cell(A) -->
    cellterm(P),
    {frame(A,cell,P,[])}.
species(A) -->
    speciesterm(P),
    {frame(A, species, P, [])}.
structure(A) -->
    structureterm(P),
    {frame(A, structure, P, [])}.
domain(A) -->
    domainterm(P),
    {frame(A; domain, P, [])}.
gene(A) -->
    geneterm (P),
    {frame(A,gene,P,[])}.
geneorprotein(A) -->
    gpterm(P),
    (X),
    \{(X = gene, frame(A, gene, P, []);
      X = protein, frame(A, protein, P, []);
      X\= gene, X \= protein, frame(A, geneorprotein, P, []))}.
aminoacid(A) -->
    aminoacidterm(P),
    {frame(A, aminoacid, P, [])}.
smallmolecule(A) -->
    smallmoleculeterm(P),
    {frame(A,'small molecule',P,[])}.
matter(A) -->
```

```
matterterm(P),
    {frame(A, substance, P, [])}.
proteinsite(A) -->
    proteinsiteterm(P),
    {frame(A, 'protein site', P, [])}.
disease(A) -->
    diseaseterm(P),
    {frame(A, disease, P, [])}.
process(A) -->
     processterm(Syn, F, Features),
     {frame(A, process, F,[]),!}.
process(A) -->
     processterm(P),
     {frame(A, process, P, {}),!}.
% terminals
proteinterm(F)
                      --> acclex(protein,F).
complexterm(F)
                      --> acclex(complex,F).
                      --> acclex(cell,F).
cellterm(F)
speciesterm(F)
                      --> acclex(species,F).
structureterm(F)
                      --> acclex(structure, F).
domainterm(F)
                      --> acclex(domain,F).
                      --> acclex(gene,F).
geneterm(F)
                      --> acclex(gp,F).
gpterm(F)
aminoacidterm(F)
                     --> acclex(aminoacid,F).
smallmoleculeterm(F) --> acclex(smallmolecule,F).
matterterm(F)
                      --> acclex(substance, F).
proteinsiteterm(F)
                      --> acclex(proteinsite,F).
                      --> acclex(disease,F).
diseaseterm(F)
processterm(F)
                      --> acclex(process, F).
% action(activate,Syn,F,Features) --> activateterm(Syn,F,Features).
activateterm(Syn,F,Features) --> acclexss(activate, Syn,F,Features).
attachterm(Syn, F, Features) --> acclexss(attach, Syn, F, Features).
breakbondterm(Syn, F, Features) --> acclexss(breakbond, Syn, F, Features).
createbondterm(Syn,F,Features) --> acclexss(createbond, Syn,F,Features).
inactivateterm(Syn,F,Features) --> acclexss(inactivate, Syn,F,Features).
                             --> acclexss(react, Syn, F, Features).
reactterm(Syn, F, Features)
                             --> acclexss(release, Syn, F, Features).
releaseterm(Syn,F,Features)
signalterm(Syn, F, Features)
                              --> acclexss(signal, Syn, F, Features).
substituteterm(Syn,F,Features)--> acclexss(substitute, Syn,F,Features).
transcribeterm(Syn, F, Features) --> acclexss(transcribe, Syn, F, Features).
promoteterm(Syn, F, Features)
                             --> acclexss(promote, Syn, P, Features).
                              --> acclexss (process, Syn, F, Features).
processterm(Syn, F, Features)
generateterm(Syn, F, Features) --> acclexss(generate, Syn, F, Features).
                              --> acclexss (cause, Syn, F, Features).
causeterm(Syn,F,Features)
% Semlist contains a phrase which is an action
actionchk(Semlist) :-
       intersect(Semlist,[attach,cause, createbond, breakbond,activate,
                 inactivate, substitute, transcribe, express, promote, signall).
```

% Semlist contains a phrase which is a connector action

```
Genome sectionc: ends here
% relations are connected by conjunctions, or
         certain 'conn' prepositions.
% Taken from MedLEE grammar to handle connectives that are conjunctions
         Ex: "severe markings, possibly from tuberculosis"
કૃ
sem relation(F,[]) -->
                       % relation and modifiers
       sem commapunc,
       sem_certainty([],C,rel),
       prepterm (P, conn),
       {frame(F, rel, P, C)}.
       %plice([[rel,P],C],R).
          Ex: "markings, swelling", "markings and swelling"
sem_relation(R,[]) --> sem_conjrel(R),
                     sem_commapunc.
          "density may represent known tumor"
    "markings, and swelling"
sem conjrel(F) -->
      sem commapunc,
      sem_conjterm(Conj),
      {frame(F, rel, Conj, [])}.
sem conjrest(Conj) -->
                        % restricted conj, has not sem relation showopt
       sem commapunc,
       sem_conjterm(Conj).
"markings, swelling"
sem_conjrest(',') -->
     snoop($0,50),
       sem commapunc,
     snoop(S,S),
      {SO } = S}.
* Treatment of Verbs from MedLEE's Grammar
            form of "be"
ŧ
sem_auxverb(B) --> sem_beterm(B).
            form of "do"
sem_auxverb(B) --> sem_doterm(B).
            form of "have"
sem_auxverb(B) --> sem_haveterm(B).
sem_recrel --> prepterm(in,_).
sem_recrel --> prepterm(to,_).
% "is not"
sem auxrel(V) --> sem auxverb(),
                sem_negterm(V).
sem_auxrel(V) --> sem_auxverb(V).
* left modifiers of findings include negation, quantity, certainty, degree, and
                                 change type modifiers
```

```
sem_integer(W) --> [W], {integer(W)}.
sem_integer(W) --> integerterm(W).
sem_timeunit(T) --> sem timeunitterm(T).
% From MedLEE grammar - "lasting 2 days", "for 2 days", "times 2 days"
sem_duration(F) -->
       sem durpreps,
       sem premeasure, %about
       sem_timemeasure(T),
       sem_durationmod, % opt. - "in duration"
       {frame(F, duration, [T], [])}.
sem_duration([],S,S).
sem_durpreps -->[times].
sem_durpreps -->
   prepterm(for,_).
sem_durpreps -->[lasting,for].
sem_durpreps -->[lasting].
sem_durpreps -->[lasted, for].
sem_durpreps -->[lasted].
sem_durationmod -->
         sem aposts, %opt. - "'s"
        [duration].
sem_durationmod --> [in], [duration].
sem durationmod --> [].
sem_aposts --> [''''], [s].
sem apost --> [].
% sem_frequency taken From MedLEE's grammar
% "two times", "times two", "two times a/per week", "two times daily"
sem frequency(F) -->
        sem_freqterm(F1), % "once"
                           % "a day"
        sem freqterm(F2),
        {frame(M, unitval, [F1, F2], []),
         frame(F, frequency, [M], [])}.
sem frequency(F) -->
        sem_freqterm(M), % "qid", "daily"
        {frame(F, frequency, M, [])}.
% "2 times",
sem_frequency(F) -->
        sem premeasure,
        sem quantityterm (M),
        sem_times,
      {frame(F, frequency, [M], [])}.
% "times 2"
sem_frequency(Q) -->
        sem times,
        sem_quantityterm(Q1),
        {frame(Q, frequency, Q1, [])}.
sem_frequency(F) -->
        [q], sem_quantityterm(Q),
             sem timeunit (T),
        {frame(F, frequency, [unitval, {Q,T]], [])}.
```

```
sem frequency(F) --> sem eachevery,
                      sem quantityterm(Q),
                      sem timeunit(T),
                     {frame(F, frequency, [unitval, [Q, T, every]], [])}.
sem_frequency(Q) -->
                        % "second"
        sem ordinal (0),
        sem_timeopt,
         {frame(Q, frequency, O, [])}.
sem_frequency([],S,S).
sem_timeopt --> [time].
sem_timeopt --> [].
sem_eachevery --> [each].
sem_eachevery --> [every].
sem times --> [times].
sem times --> [x].
% Taken from MedLEE's grammar
negation modifier - "no" as in "no cardiomegaly"
sem_negation(F) -->
        sem negterm(N),
         {frame(F, neg, N, [])}.
% negation not present
sem_negation([],S0,S0).
% Taken from MedLEE's grammar
% quantity modifier - "two" as in "two masses"
sem_quantity(F) -->
       snoop(S0,S0),
        { \+ checkst(sem_dates,1,s,_,SO,_) }, % not a legitimate date
       sem_quantityterm(Q),
       sem quantityrmod(),
                                   % "2 or 3", "2 to 3"
        { \+ next wordunit($0),
                                   % rule out '2 mm'
        frame(F, quantity, Q, [])
sem_quantity([],S0,S0).
sem commapunc([', '|S],S).
sem_commapunc(S,S).
sem_conjterm(C)
                     --> acclex(conj,C).
sem_doterm(D)
                     --> acclex(vdo,D).
sem endmark([.|S],S).
sem_endmark([;|S],S).
sem_freqterm(F)
                     --> acclex(freq,F).
sem_haveterm(H)
                     --> acclex(vhave, H).
integerterm(I)
                     --> acclex(integer,I).
sem measureterm(M) --> acclex(unit,M).
sem_medterm(M)
                     --> acclex(med,M).
sem negterm(N)
                     --> acclex(neg,N).
prepterm(P,C)
                     --> acclex(p, [P,C]).
sem timeunitterm(T) --> acclex(timeunit,T).
```

```
% lexog - adapted from MedLEE lexicon
፟ቔቔ፟ቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔ CLOSED WORD CATEGORY LEXICON ቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔቔ
8888888888888888888
                        NEGATIONS
                                  :-unknown(_,fail).
:-multifile(wdef/3).
wdef(cannot, neg, no).
wdef (neither, neg, no).
wdef (never, neg, no).
wdef (no, neg, no).
wdef (non, neg, no).
wdef (none, neg, no).
wdef (not, neg, no).
wdef (nothing, neg, no).
****************
                        wdef('&',conj,and).
wdef('/',conj,or).
wdef('-',grammar,'-').
wdef('+',conj,and).
wdef(although,conj,and).
wdef (and, conj, and).
wdef(as,conj,and).
wdef (because, conj, and).
wdef (but, conj, and).
wdef(',',conj,',').
wdef(except,conj,no).
%wdef(if,grammar,if).
wdef(minus,conj,no).
wdef(nor,conj,no).
wdef(or,conj,or).
wdef(that, grammar, that).
wdef(though,conj,and).
wdef (thru, conj, and).
wdef (verses, conj, or).
wdef (versus, conj, or).
wdef(vs,conj,or).
wdef (when, grammar, when).
wdef (where, grammar, where).
wdef (whereas, conj, and).
wdef (which, grammar, which).
wdef (while, conj, and).
wdef (who, grammar, who).
wdef (yet, conj, and).
$$$$$$$$$$$$$$$$$$$$$$$ PREPOSITIONS $$$$$$$$$$$$$$$$$$$$$$$$
wdef(above,ploc,above).
wdef(about,p,[approximately,nconn]).
wdef(about,ploc,about).
wdef (across, ploc, across).
wdef(abutting,ploc,near).
wdef(accompanies,p,[with,conn]).
wdef(accompanying,p,[with,conn]).
wdef(adjacent,ploc,adjacent).
wdef (adjacent, region, adjacent).
wdef(after,p,[after,conn]).
wdef(after,tprep,after).
wdef(along,p,[on,nconn]).
wdef(approximately,p,[approximately,nconn]).
wdef(around,p,[approximately,nconn]).
```

```
wdef(at,p,[at,nconn]). .
wdef(atop,p,[on,nconn]).
wdef(before, ploc, before).
wdef (before, tprep, before).
wdef (behind, ploc, behind).
wdef (below, ploc, below) .
wdef (between, ploc, between).
wdef (beyond, ploc, beyond).
wdef(by,ploc,near).
wdef(despite,p,[with,conn]).
wdef (during, p, [during, conn]).
wdef (during, tprep, during).
wdef (encasing, ploc, encasing).
wdef(extending,p,[in,nconn]).
wdef(following,p,[after,conn]).
wdef(following,tprep,after).
wdef(for,p,[for,nconn]).
wdef(from,p,[from,conn]).
wdef(in,p,[in,nconn]).
wdef(including,p,[with,conn]).
wdef(into,p,[in,nconn]).
wdef(involving,p,[of,nconn]).
wdef(next,tprep,next).
wdef(occupying,p,[in,nconn]).
wdef(on,p,[on,nconn]).
wdef(of,p,[of,nconn]).
wdef(over,ploc,over).
wdef(overlie,ploc,over).
wdef(overlied,ploc,over).
wdef (overlies, ploc, over).
wdef(overlying,ploc,over).
wdef (prior, tprep, before).
wdef(near,ploc,near).
wdef (radiating, ploc, radiating).
wdef(regarding,p,[about,nconn]).
                                   % 'roughly 6 mm'
wdef(roughly, grammar, roughly).
wdef(since,p,[since,conn]).
wdef(since, status, subsequent).
wdef(through,p,[in,nconn]).
wdef(throughout,p,[in,nconn]).
wdef(to,p,[to,nconn]).
wdef(toward,p,[to,nconn]).
wdef(towards,p,[during,conn]).
wdef (under, ploc, below).
wdef (underneath, ploc, below).
wdef(until,tprep,until).
wdef(up,grammar,up).
wdef(upon,p,[on,nconn]).
wdef(via,p,[with,conn]).
wdef(with,p,[with,conn]).
wdef(within,p,[in,conn]).
wdef(without,p,[no,conn]).
%wdef(without, neg, no).
wdef('%',unit,percent).
```

```
wdef(cc,unit,cc).
wdef (centimeter, unit, cm).
wdef(centimeters, unit, cm).
wdef(cm, unit, cm).
wdef (degrees, unit, degree).
wdef(gm,unit,gram).
wdef (gms, unit, gram).
wdef (gram, unit, gram).
wdef (grams, unit, gram).
wdef(kg,unit,kilogram).
wdef(kilo,unit,kilogram).
wdef(kilogram, unit, kilogram).
wdef(kilograms, unit, kilograms).
wdef(liter,unit,liter).
wdef(liters, unit, liter).
wdef (microgram, unit, microgram).
wdef (micrograms, unit, microgram).
wdef(milliliter,unit,ml).
wdef(milliliters,unit,ml).
wdef(milligram, unit, mg).
wdef (milligrams, unit, mg).
wdef(milliseconds.unit.millisecond).
wdef(millivolts,unit,millivolt).
wdef(ml,unit,ml).
wdef (millimeter, unit, mm).
wdef (millimeters, unit, mm).
wdef(mm, unit, mm).
wdef(ozs,unit,ounce).
wdef (percent, unit, percent).
告告告告答·查告告诉者者是否有责任者的基本的主要,NUMBERS 专家员的专家员员会员会员员的责任者的责任者的责任者的责任者的责任者的责任者
wdef(half,integer,'one half').
wdef(semi, quantity, semi).
wdef(ii,integer,2).
wdef(iii,integer,3).
wdef(vi,integer,4).
wdef(v,integer,5).
wdef(vi,integer,6).
wdef(vii,integer,7).
wdef (viii, integer, 8).
wdef(ix,integer,9).
wdef(xii,integer,12).
wdef(xiii,integer,13).
wdef (one, integer, 1).
wdef(two,integer,2).
wdef (double, quantity, double).
wdef(three,integer,3).
wdef (four, integer, 4).
wdef (quadruple, quantity, quadruple).
wdef(five,integer,5).
wdef(six,integer,6).
wdef(sixty,integer,60).
wdef (seven, integer, 7).
wdef(eight,integer,8).
wdef(nine,integer,9).
wdef(ten,integer,10).
wdef(eleven,integer,11).
wdef(twelve,integer,12).
```

```
wdef (thirteen, integer, 13).
wdef (fourteen, integer, 14).
wdef (fifteen, integer, 15).
wdef(sixteen,integer,16).
wdef (seventeen, integer, 17).
wdef (eighteen, integer, 18).
wdef (nineteen, integer, 19).
wdef (twenty, integer, 20).
wdef(thirty,integer,30).
wdef(forty,integer,40).
wdef(fifty,integer,50).
wdef(sixty,integer,60).
wdef(seventy,integer,70).
wdef(eighty,integer,80).
wdef(ninety,integer,90).
wdef (hundred, integer, 100).
wdef(thousand,integer,1000).
wdef(million,integer,1000000).
wdef(billion,integer,billion).
wdef(zero,integer,0).
wdef(first,ointeger,1).
wdef(second,ointeger,2).
wdef(third,ointeger,3).
wdef (fourth, ointeger, 4).
wdef(fifth,ointeger,5).
wdef(sixth,ointeger,6).
wdef(seventh,ointeger,7).
wdef(eighth,ointeger,8).
wdef(ninth,ointeger,9).
wdef (tenth, ointeger, 10).
wdef (eleventh, ointeger, 11).
wdef (twelvth, ointeger, 12).
wdef(thirteenth,ointeger,13).
wdef (fourteenth, ointeger, 14).
wdef(fifteenth,ointeger,15).
wdef(sixteenth,ointeger,16).
wdef(seventeenth,ointeger,17).
wdef (eighteenth, ointeger, 18).
wdef (ninteenth, ointeger, 19).
wdef(triple, quantity, triple).
wdef(twentieth,ointeger,20).
wdef (thirtieth, ointeger, 30).
wdef(single, quantity, 1).
wdef(solitary, quantity, 1).
wdef(frequency,grammar,frequency).*/
wdef 🦰 .', grammar, '.').
.wdef(';',grammar,';').
wdef('/',grammar,'/').
wdef(':',grammar,':').
wdef('?', certainty, 'moderate certainty').
wdef('+',certainty,'high certainty').
wdef('''',grammar,'''').
wdef (once, freq, 1).
wdef(times, grammar, x).
```

wdef(twice, freq, 2).

```
% lexicon with lex0g containing common English words adapted from lex0 of
 MedLEE%
 % lexig from lex1 of MedLEE
 % August 23, 1999
 . CAROL FRIEDMAN
                                                                        *
           QUEENS COLLEGE, COLUMBIA UNIVERSITY
                                                                        ŧ
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 홪
                     Version 3.0 4-01-00
                       Version 2.0 1-31-96
                       Version 1.0 1-5-92
                       SEMANTIC LEXICON FOR CLINICAL TEXT
 ş.
 ¥
 ¥
    The lexicon consists of several files:
 者
       lex0g.pl: single word closed classes
 욯
       lexig.pl: single word - general modifier type words:
 용
      wdef(category,target).
          word - is the name of the word being categorized;
          category - is the semantic category for the word
          target - is the canonical/standard form for the word
                      words which are synonyms should be assigned the same
                      canonical form.
     multi-word phrases are categorized as follows:
                                                                         윷
                                                                         용
     phrase (word, category, phrase, target).
                                                                        ક્ષ
                                                                         욯
    Semantic Categories:
         certainty "possible"
                canonical values limited to: moderate - for possible
 £
                                            high - for high possible
 ę.
                                            low - for low possible
        conj - relational operators "and", "or", which connect one finding %
               to another finding
         neg - negation "no", "not"
         quant - for quantitative information "many"
 *
 :-unknown(_,fail).
:-ensure_loaded([nsphrase,lex0g,lex1g,lexsemact,lexsyn,lexsub]).
```

*/

```
% definitions kept from MedLEE lexicon - lex1.pl
wdef(be, vbe, 'high certainty').
wdef(been, vbe, 'high certainty').
wdef(being, vbe, 'high certainty').
wdef(was, vbe, 'high certainty').
wdef(is, vbe, 'high certainty').
wdef(were, vbe, 'high certainty').
/*
wdef (became, vcertainty, 'high certainty').
wdef (become, vcertainty, 'high certainty').
wdef (becomes, vcertainty, 'high certainty').
wdef(becoming, vcertainty, 'high certainty').
                             put in action lexicon
wdef (changed, change, change).
wdef (changes, change , change) .
wdef (changing, change, change).
wdef(necessarily,certainty,'high certainty').
wdef (necessary, vrecommend, recommended).
wdef (necessitate, vstatus, need).
wdef (necessitated, vstatus, need).
wdef(necessitating,vstatus,need).
wdef (necessitates, vstatus, need).
wdef (need, vstatus, need).
wdef (needed, vstatus, need).
wdef (needing, vstatus, need).
wdef (needs, vstatus, need).
```

28

```
% file ml_parser.pl
:- multifile(phrase/5).
:- multifile(wdef/3).
:-unknown(_,fail).
% Load in program components - library components are part of Prolog
:- ensure loaded([library(basics),library(not),library(lists),
   library(readin), library(strings), library(ctypes), library(readconst),
   library(date), library(listparts), library(sets),
   radrec, radpardb, useful, util, tagging, lexicon, gengram]).
%: - initialization run.
%run :- on exception(Error, processrun, stop(Error)).
runtime_entry(start) :- processrun.
runtime_entry(abort) :- halt.
% process report
processrun :- process, halt.
%stop(Error) :-
    told,
    write(user error, 'Error: '), write(user_error, Error), halt.
% get user supplied parameters and process report
process :-
get_args(Mode,Infile,Outfile,Prb,Undefs,Protocol), !,
           (Examtype = []; % must have a domain
            process (Infile, Outfile, Prb, Undefs)).
% open Infile (text input) and process
process(Infile,Outfile,Prb,Undefs) :-
           see(Infile), seen, see(Infile),
           on_exception(Error,
           test_genome(Outfile, Prb, Undefs),
               app erro( ,Outfile,Error)),
           closefiles (Outfile, Prb, Undefs).
process(_,Outfile,_,_) :-
        app_err(_,Outfile,'Program failed').
app_err0(_,Output,Error) :-
       tell(Output),
       write('<error>'),
       write('Prolog Error occurred: '),
       app_err(_,Output,Error).
app_errl(_,Output,Error) :-
       tell(Output),
       write('<error>'),
       write('Error in input: '),
       app_err(_,Output,Error).
app_err(_,Output,Error) :-
       tell(Output),
       write(Error), write('</error>'), nl.
closefiles (Outfile, Errfile, Unfile) :-
      tell(Outfile), told,
      (Errfile = []; tell(Errfile), told),
      (Unfile = []; tell(Unfile), told).
```

```
% Argument options - get user defined arguments
% -p ProbFile (otherwise default is problem messages are not written to file)
% -i Infile (if input is supplied by file and not standard input
% -s Section (default is impression)
% -m Mode (default is relax; the three choices are strict, relax, skip)
% -o Outfile (if output should be file and not standard output)
% -? Provide list of default arguments
% -u Undefs (otherwise default is - undefined messages are not written
용
      to a file)
get_args(Mode,Infile,Outfile,Prbfile,Undefs,Protocol) :-
    unix(args(Args)),
  (Args = [], !, writesyntax;
  Args = ['?'],!, writesyntax;
Args = [X|Rest], !,
   set_args([X|Rest], Mode, Infile, Outfile, Prbfile, Undefs, Protocol)).
writesyntax :-
     write(user_error, 'geneparser [-m Mode)'),
     nl (user_error),
     write(user_error,'
                                  [-t Outtype] [-p Probfile] [-u Undefs]'),
     nl (user_error),
     write(user_error,'
                                [-i Infile] [-o Outfile]'),
     nl (user error).
```

PCT/US00/10302 WO 00/63687

```
% nsphrase.pl - contains words/phrases that are ignored
nosem(both, [both]).
nosem(however, [however]).
nosem(selectively, [selectively]).
nosem(specifically, [specifically]).
nosem(the, [the]).
nosem(a, [a]).
```

```
% file radpardb.pl
% June 25, 1999
% fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=, \sim=]). % same priority and type as = or ==
:- dynamic(sentno/1).
% \sem\radpardb.pl
*parse_sentences(+Beg,-Fmt,-ParseErrors,-Undefineds,-Unsents,+Section,
                 +UserMode, +Examtype, Sentno, Outsno, IncSno)
        Beg is list of sentences, Fmt is list of target forms,
욯
        ParseErrors are a list of sentences which could not parse,
        Undefineds is a list of undefined words in sentence
        Unsents is a list of sentence containing undefined words
        Section is the section of the examination, UserMode is the
        parsing mode specified by user,
        Examtype is the domain (type of exam)
ę.
        Sentno is the number of the starting sentence
        Outsno is the last sentence number + 1
        IncSno is the amount that the sentence number should be increased
             (i.e. it is 1 when called by parse_sects and 0 when in
               recovery mode)
     Each sentence is parsed independently.
parse_sentences([],[],[],[],[],_,_,_,_,) :- !. %no more sentences
parse_sentences(Beg,Fmtlist,Outfail,Outundefs,OutunSents,
                 Section, UserMode, Examtype, _, _, IncSno) :-
    get_sentence(Beg,S,Rest), !,
    ( isidentifier(S), !, % ignore identifier sentences - parse remainder
      parse sentences (Rest, Fmt1, Outfail, Outundefs, OutunSents,
                 Section, UserMode, Examtype, _, _, IncSno), !,
       (outputform(htext), S \= ['.'], !, IncSno \= 0, %0 means in recovery
mode
        append([[[sentence,S]]],Fmt1,Fmtlist);
        Fmtlist = Fmtl
      %( IncSno = 0, !; % on same sentence in recovery mode
      % sentno(Sno), NewSentno is Sno + IncSno,
% retract(sentno(_)), assert(sentno(NewSentno))
      88),
    % Incsno = 1, write('***'), write_list(S,3,_), nl, !,
     % Incsno = 0,
      preprocess(S,Bs,Undef,Semlist,strict), % bracket and check for undefineds
      parse_modes(S,Bs,Semlist,Fmt1,Errors,Undef,Unsents,Section,Writefail,
                  Examtype, UserMode, IncSno), % parse first sentence
      parse_sentences(Rest,Fmt2,Moreerrors,Moreundefs,MoreUnSents,
                  Section, UserMode, Examtype, _, _, IncSno), % parse remaining
      append(Errors, Moreerrors, Outfail),
                                               % Combine failures
      (outputform(htext),
            (Fmt1 = [], IncSno = 0,
             !, append([Fmt1],Fmt2,Fmtlist); % add extra bracket for 1st
             Fmt2 = [], Fmtlist = Fmtl , !
```

```
append (Fmt1, Fmt2, Fmtlist)
              % Combine targets
      append (Unsents, MoreUnSents, OutunSents), % Combine sentences
      append (Undef, Moreundefs, Outundefs)
                                          % Combine undefined words
%parse_modes(+S,+Bs,+Semlist,-Fmt,-Failures,+Undef,-Unsents,+Section,
     +WriteMessage, +Examtype, +Mode, +IncSno)
        S is original sentence; Bs is sentence after lexical lookup
왐
        Semlist is list of semantic categories in sentence
ક
        Fmt is formatted output,
        Failures is list of sentences/fragments which could not be parsed.
者
š
        Undef are words not in lexicon, Unsents are sentences containing
                undefined words
        Section is name of section being processed
        WriteMessage is message returned from doresult (in case doresult fails)
g.
        Examtype is domain, Mode is user specified mode
        IncSno is 0 if this is a fragment of a sentence that was already
                parsed - but unsuccessfully; is 1 if this is a new sentence
* Best possible - try to get the most accurate parse possible trying
% all alternative strategies in turn if neccessary
% All words in sentence are defined
parse modes (S, Bs, Semlist, Fmt, Errors, [], [], Section, no, Examtype, Pmode,
      (Pmode = bpseg, Pmodemod = mode2, !; %in recovery mode
       Pmode = bpseg2, Pmodemod = mode2, !;
       Pmode = bpseg3, Pmodemod = mode2, !;
       Pmode = bpskip, Pmodemod = mode4, !; %in recovery mode
        % in user specified parse mode - don't parse in mode 5 or keyword
       Pmode \= keyword, Pmode \= mode5,
       Pmodemod = model
      ).
      dosent(S,Bs,Semlist,Fmtl,Message,Section, ,Examtype,Pmodemod,_),!, %
strict first
      recovery(_,S,Bs,Semlist,Fmt2,Message,Errors,[],[],Section,
                 Pmode, Examtype, _), % try alternative modes if neccy
      (outputform(htext), Inc \= 0, !, append([[[sentence,S]],Fmt1,Fmt2],Fmt);
       append (Fmt1, Fmt2, Fmt)
      ١.
% alternative strategies if have undefined words
parse_modes(S,Bs,Semlist,Fmt,Errors,Undef,Unsents,Section,no,Examtype,
             Pmode, Inc) :-
     Undef \= [],
     recovery(_,S,Bs,Semlist,Fmt1,yes,Errors,Undef,Unsents,Section,
                Pmode, Examtype, _), % try alternatives if have undefineds
     (outputform(htext), Inc/= 0, !, append([[sentence,S]],Fmt1,Fmt);
     Fmt = Fmt1
     ) .
% key word strategy is fastest but least reliable;
parse_modes(S,Bs,Semlist,Fmt,Errors,Undef,Unsents,Section,no,Examtype,
             Pmode, Inc) :-
    (Pmode = keyword; Pmode = mode5
     ; Pmode = mode5),
    recovery (5, S, S, Semlist, Fmtl, yes, Errors, Undef, Unsents, Section, Pmode,
               Examtype,_),
     (outputform(htext), Inc \= 0, !, append([[sentence,S]],Fmt1,Fmt);
```

```
Fmt1 = Fmt
% Parsing/Recovery modes
% parse_modes(+Level,+S,+Bs,+Sem,-Fmt,+Failed,+Undef,+Unsents,+Section,
              +Pmode, +Examtype, _)
    Level is the recovery level of the predicate
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    S is the original sentence list
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   Bs is the
ક
   Sem is the list of semantic categories in the sentence
   Fmt is the formatted output for the sentence
ž
¥
   Failed is 'yes' if the parse was unsuccessful, and 'no' otherwise
   Undef is a list of words in sentence which are undefined(not in lexicon)
£
Š
   Unsents are the lists of sentences/segments which could not be parsed.
   Section is the section of the report
¥
욯
   Pmode is the user specified parse mode
  Examtype is the domain
% mode 1 is the strictest parsing mode - the parser succeeded for the complete
         original sentence using the grammar; all words in original sentence
         are defined in lexicon
$ mode 1 - alternative not needed because parse succeeded
recovery(1,_,_,[],no,[],Undef,Unsents,_,_,_) :-!.
         - no alternative strategy allowed in mode 1
            in case where there are no undefineds, Noparse is S
recovery(1,S,_,_,[],yes,S,[],[],_,Pmode,_,_) :-
         Pmode = strict; Pmode = model, !.
           in case there are undefineds, Unsents is S
recovery(1,S,_,_,[],yes,Noparse,Undef,Unsents,_,Pmode,_,_) :-
        (Pmode = strict; Pmode = 'model'),
        Undef \= [], Unsents = S, Noparse = [], !.
recovery(1,S,_,Semlist,[],yes,S,_,_,_,_,_) :-
sentence contains no relev. information, don't try to recover
     \+ (subtype(finding,Semlist); subtype(time,Semlist)), !.
% mode 4 - skip undefined words and try to parse according to mode 1
recovery(4,S,_,_,Fmt,yes,Errors,Undef,[],Sect,Pmode,Examtype,_) :-
         Undef \= [],
         (Pmode = bp; Pmode = mode4;
          Pmode = bpseg; Pmode = bpskip; Pmode = mode4
         preprocess(S,Bs, ,Semlist,bpskip),
         dosent(S,Bs,Semlist,Fmt1,Message,Sect,_,Examtype,mode4,_),!,
         recovery(_,Bs,Bs,Semlist,Fmt2,Message,Errors,[],[],Sect,
                     bpskip, Examtype, Sentno), % try alternatives if neccy
           append(Fmt1,Fmt2,Fmt).
% mode 3 - try longest parsed segment; partition rest of
            sentence using mode 5 for parse mode bp
recovery (3, S, Bs, ,Fmt, yes, Errors, Undef, Unsents, Sect, Pmode, Examtype, _) :-
         % allowable modes for choosing longest segment
         (Pmode = bp; Pmode = bpskip;
          Pmode = skip; Pmode = mode3; Pmode = mode4;
          Pmode = bpseg3; Pmode = bpseg
         (Pmode = bpskip, Pmodemod = mode4 3;
        Pmodemod = mode3
        ),
         checkst(sem pattern, ,s, Target, Bs, Rest), %check symbol table
```

```
$dooresult(Target, Fmt1, Examtype, Sect, Pmodemod, _).
         formatresult (Target, Pmodemod, Fmt1),
         (Pmode = mode3, Fmtlist = [], Errors = Rest;
         recovery(5, Rest, Rest, _, Fmtlist, yes, Errors, Undef, Unsents, Sect,
                        Pmode, Examtype, )
         append (Fmt1, Fmtlist, Fmt).
% mode 2 segments sentence using word barrier methods. This mode is tried if
           parse failed for original sentence/or there are undefined words
            segment sentence using word barriers
recovery(2,S,_,_,Fmt,yes,Errors,Undef,Unsents,Sect,Pmode,Examtype,_) :-
         (Pmode = bp; Pmode = bpskip; Pmode = mode2; Pmode = skip;
          Pmode = mode2; Pmode = mode3; Pmode = mode4;
          Pmode = bpseq; Pmode = bpseg2;
          Pmode = bpseg3
         segmentandparse(S,Fmt,Errors,Unsents,Sect,Pmode,Examtype,_),!.
% mode 5 - try to partition sentences by findings
% when a finding in sentence is found, go left until first
    modifier is found (if 2 findings are next to each other, 2nd one
    is considered the finding and 1st is considered the modifier)
    Repeat searching for successive findings using this method
recovery(5,[],[],_,[],_,[],_,_,_,_,_) :- !.
recovery(5,S,Bs,_,Fmt,yes,Errors,Undef,Unsents,Sect,
               Pmode, Examtype, _) :-
         (Pmode = bp; Pmode = bpskip; Pmode = bpseg; Pmode = keymode;
          Pmode = mode5; Pmode = negmode
          preprocess(S,Bs1,_,_,bpskip), % skip undefined words
          actionfindingseg(Bs1,Fseg,Before),!, % get segment containing finding
          (Fseg = [], Errors = S, !; % no finding to segment
           $Before = [], Errors = Bs, Fmtl = [], !; % this part was tried
           preprocess (Fseg, Bseg, , Semlist, bpskip),
           dosent (Fseg, Bseg, Semlist, Fmt1, Message, Sect, _, Examtype,
                   mode5,_) % try to parse finding segment
           (Before = [], Before1 = [], Message = yes, !; % no segmenting yet -
skip beg.
            Message = yes, Beforel = Before, !; %don't add '.'; have to skip
more
            append(Before,['.'],Beforel)
           ),
           ( Fseg = [], Fmt = [], !; % no finding left in sent. - don't recover
           recoverrest (Fseg, _, Beforel, Fmt2, Message, Errors,
                     Sect, Newmode, Examtype, ),
            % recover remainder
            append (Fmt1, Fmt2, Fmt)
% nothing could be recovered; all input -> Errors ; Format is []
recovery(_,Sents,_,_,[],yes,Sents,Undef,[],_,_,_).
% part of phrase was skipped, add period and treated skipped part as a
% sentence
% recoverrest(+Segment,+Semlist,+Before,-Fmt,+Message,-Failures,+Section,
        +Mode, +Examtype, )
        Segment is part of sentence with a finding
```

```
Semlist is a list of semantic categories for that sentence part
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        Before is the part of sentence before Segment
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        Fmt is the format for this segment
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용
        Message is 'no' if there is no segmantic information to be recovered
                Message is 'yes' otherwise
å
        Failures are lists of segment(s) that could not be parsed successfully
욯
۶
        Section is section being processed, Mode is user specified parsing mode
        Examtype is domain
recoverrest(_,_,Before,[],no,Beforel,_,_,_,) :-
  (Before = [], Before1 = [], !; % nothing was skipped
   append(Before,['.'],Before1)
% nothing left to recover; write phrase that was skipped
recoverrest([],_,Before,[],yes,Before1,_,_,_) :-
   (Before = [], Before1 = [], !;
   append(Before,['.'],Beforel)
   ), !.
% can recover partial parse
recoverrest (Bs, ,Before,Fmt,yes,Errors,Sect,Pmode,Examtype,_) :-
         checkst(sem_pattern,_,s,Target,Bs,Restseg), % recover from symbol tab.
         $doresult(Target,Fmt1,Examtype,Sect,mode5,_),
          formatresult(Target, mode5, Fmt1),
         recovery(5, Restseg, Rest, _, Fmt2, yes, Error2,
                    [], [], Sect, Pmode, Examtype, _),
         append (Fmt1, Fmt2, Fmt),
         (Before = [], Errors = Error2, !;
                                            %nothing skipped to add '.' to
          append(Before, ['.'|Error2], Errors)
% cannot recover partial parse - skip first element and retry
% if 1st element is a negation semantic type, skip 2nd element instead
¥
      Handles case where 1st element is a negation, certainty or status
        add 2nd element to unparsed sentences list (enlcosed in angle brackets).
*
recoverrest([X,Y|Restseg],_,Beforel,Fmt,yes,Errors,
                     Sect, Pmode, Examtype, ) :-
         foundword(X,Sem1,Tar),
         ( member(Sem1, [neg, certainty, vcertainty, vconn, status, vstatus]);
           Sem1 = p, Tar = [,conn]
         % (Mod = neg; Mod = certainty; Mod = status; Mod = vcertainty), % leave
this mod in
          preprocess([X|Restseg],Fseg0,_,_,bpskip), % skip undefined words
          findingseg(Fseg0,Fseg,Before2), !, % get finding seg
          (Fseg = [], Errors = [X,Y|Restseg], Fmt = []; % no finding
           preprocess(Fseg,Bseg,_,Restsem,bpskip), % skip undefined words
           dosent(Fseg,Bseg,Restsem,Fmt1,Message,Sect, ,Examtype,
                   mode5,_), % try to parse finding segment
           recoverrest(Fseg,_,[Y|Before2],Fmt2,Message,Error2,
                    Sect, negmode, Examtype, _), % recover remainder
           (Before1 = [], Errors = Error2, !;
            append(Before1,[.|Error2],Errors)
           ).
           append (Fmt1, Fmt2, Fmt)
   skip 1st element; enclose it in brackets
recoverrest([X|Restseg],_,Beforel,Fmt,yes,Errors,
                Sect, Pmode, Examtype, _) :-
          preprocess(Restseg,Fseg0,_,_,bpskip),
```

```
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                                                                 PCT/US00/10302
          findingseg(Fseg0, Fseg, Before2), !, % get finding seg
          append (Before1, [X | Before2], Before),
          (Fseg = [], Errors = [X | Restseg], Fmt = []; % no finding
           preprocess(Fseg,Bseg,_,Restsem,bpskip),
          dosent (Fseg, Bseg, Restsem, Fmt1, Message, Sect, _, Examtype,
                    mode5,_), % try to parse finding segment
          recoverrest (Fseg, _, Before, Fmt2, Message, Errors,
                      Sect, Newmode, Examtype, ), % recover remainder
          append(Fmt1,Fmt2,Fmt)
          ١.
% no semantic information left; return Errors
recoverrest([X|Restseg],[],Before1,Fmt,yes,[X|Restseg],
                Sect, Pmode, Examtype, _).
%dosent(+S,+Bs,+Semlist,-Fmtlist,+Message,+Section,+WriteMessage,+Examtype,
¥
        +Mode)
       S is original list of words in sentence; Bs is list after lexical lookup
용
       Semlist is list of semantic categories corresponding to Bs
       Fmtlist is list of target forms for sentence
       Message is 'yes' if the output from parser signals a failure,
                and 'no' otherwise
       Section is section of examination being processed
       WriteMessage signals whether an error occurred in generating target form
       Examtype is the domain, and Mode is the user specified mode of parsing
% Parse sentence and returns target in nested format
% Handles case where sentence should be skipped because info is about
    family member or peripheral to patient
dosent(S,_,Semlist,[],Error,_,_,_,_) :-
  skipsentence(S, Semlist, Error), !.
dosent(S,Bs,Semlist,Fmtlist,Errormsg,Section,Writefail,Examtype,Mode,_) :-
   attemptparse (P, Bs, sentence, Semlist, Section, Atotal),
   ( P = [failure], Errormsg = yes, Writefail = no, ! % parse failure
      P = [], Errormsg = no, Writefail = no, Fmtlist = [], ! % empty target
      %doresult(P,Fmtlist,Examtype,Section,Mode, ),
        formatresult (P, Mode, Fmtlist),
        Errormsg = no, Writefail = no,!
      Errormsg = yes, Writefail = yes, !
   ) .
%parse_sentences(Beg, Beg, [], [], _, _, _) :- !.
% attemptparse(-P,+Bs,+Structure,+Semlist,-Ftype,-Total)
        P is output from parser
        Bs is list of words in sentence after lexical lookup
        Structure is name of structure to be parsed
        Semlist is list of semantic categories corresponding to elements in Bs
        Total is number of times parser reached sem_sent in grammar;
                 where sem_sent is highest level predicate in grammar
% don't parse if sentence consists of only '.' or ';'
attemptparse([],Bs,_,_,_,) :-
   Bs = ['.']; Bs = [';'].
```

* if a template exists for whole sentence, get parse from it

```
attemptparse(P,Bs,sentence,_,_,_) :-
   Bs = [X,','], is_list(X), % the whole sentence is a finding
   find sem sent(P,X), !.
% parses and retracts wellformed string table - parses sentence
attemptparse(P,Bs,sentence,Semlist,Ftype,Atotal) :-
   retractall(wfst(_,_',_',_'_,'_)),
   retractall(addstotal()),
   sem sent(P, Semlist, Atotal, Bs, []), !.
% parses and retracts wellformed string table - parses bodypart only
attemptparse(P,Bs,bodypart,_,_,_) :-
   sem bodyloc(P,Bs,[]),
   retractall(wfst(_,_,_,_,_)), !.
*segmentandparse(+Sentences,-Fmtlist,-Failures,-Unsent,+Section,+Mode,
        +Examtype, +Sentno)
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        Sentences is list of sentence segments.
        Fmtlist consists of the formatted output for the segments
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¥
        Failures is the list of unparsed segments.
        Unsent is the list of segments with undefined words.
        Section is the section being processed, Mode is the user specified mode
        Examtype is the domain and Sentno is the sentence id.
segmentandparse([],[],[],[],_,_,_) :- !.
segmentandparse(Sentences,Fmtlist,Failures,UnSent,Section,Mode,
                   Examtype, Sentno) :-
     get_sentence(Sentences,S,Rest), !, %sentence to segment
     preprocess(S,S1,_,Semlist,Mode), !,
     (Mode = mode2, NewPmode = bpseg2, !;
      Mode = mode3, NewPmode = bpseg3, !;
      NewPmode = bpseg
     ),
     ( segment1(S1, Segs, [], seg), !,
         parse sentences (Seqs, Fmt1, Fails, ,Un1, Section, NewPmode, Examtype,
                            Sentno, Sentno, 0), !
      ; segment2(S1, Segs, [], seg), !,
         parse_sentences(Segs,Fmt1,Fails,_,Un1,Section,NewPmode,Examtype,
                            Sentno, Sentno, 0), !
      ; segment3(S1, Segs,[], Negstatus, seg), !,
         parse_sentences (Segs, Fmt1, Fails, _, Un1, Section, NewPmode, Examtype,
                            Sentno, Sentno, 0), !
       % fails if cannot segment sentence; otherwise segments remainder
      segmentandparse (Rest, Fmt2, Nexterrors, NextUns, Section, Mode,
                         Examtype, Sentno),
      append (Fmt1, Fmt2, Fmtlist),
      append (Un1, NextUns, UnSent),
      append (Fails, Nexterrors, Failures), !.
%segment1(+S,-Segs,+Beg,+Message)
¥
        S is list of words in sentence
        Segs consists of sentence segments as separate sentences
욯
        Beg is list of words in sentence prior to the current portion of sentenc
왐
        Message is 'seg' if segmenting succeeded and 'noseg' otherwise
segment1([],[],_,noseg) :- !.
% segment sentence at connect phrase/word or at most conjunctions
% if negation precedes, restore negation
```

```
segment1([X Rest],['.','<eos>' Rem], Beg, seg) :-
     \+ sem_endmark(Rest,[]), % don't segment if at end already
    ( X = nor, append([no],Rest,Rem) % ok to segment at nor
     ;X = without, append([no],Rest,Rem) % ok to segment at without
     %:X = ':', Rest = Rem
      ; Sem = neg, Rest = [Next|Rest2], % have negation; test word after
        foundword(Next,Sem2,Target2), % for connective - add back negation
         testforconn(Next, Sem2, Target2), Rem = {X | Rest2}
     ; testforconn(X, Sem, Target), Rest = Rem
    ) .
segment1([X|Rest],[X|Newrest],Start,Seg) :-
       append(Start, [X], Beg), % part before segmentation
       segment1 (Rest, Newrest, Beg, Seg).
testforconn(X,Sem,Target) :-
     ( Sem = p, Target = [P,conn], P\= with % segment at connective prep
      ; member(Sem, [vconn, vshow]) % segment at these types of verbs
      ; Sem ≈ conj, \+ member(X, [and, or, ', ', '/', as])
     ) .
% segment at certain words -
segment2([],[],(],noseg) :- !.
segment2(S,Segs,[],seg) :-
        seq2 (S, Rest, Seqs),
        \+ sem endmark(Rest,[]), !.
segment2([X|Rest],[X|Newrest],[],Seg) :-
       segment2 (Rest, Newrest, [], Seg).
seg2([X|Rest],Rest,['.','<eos>'|Rem]) :-
        member (X, [which, that, until, where, when, while, who,
         '(',')', between, whereby, after, before, prior,
         greater, ranging]),
        Rem = Rest, !.
segment3([],[],_,_,noseg) :- !.
% segment at conjunction - if negation preceded conjunction, add
segment3([X|Rest], Rem, Beg, Negstatus, seg) :-
       \+ sem_endmark(Rest,[]), !, % already at end of sentence
        seg3([X|Rest], Rem, Beg, Negstatus, seg), !.
seg3([X|Rest],Rem,Beg,Negstatus,seg) :-
        wdef(X,conj,_),
        member(X, [and, or, ', ']),
        (nonvar(Negstatus), Rem = ['.', Negstatus|Rest], ! %restore negation
        ; Rem = ['.','<eos>'|Rest], !
seg3([X|Rest],[X,'.','<eos>'|Rest],_,_,seg) :-
       foundword(X,age), !.
seq3([X|Rest],[X|Newrest],Start,Negstatus,Seg) :-
        ( nonvar(Negstatus), !; % 1st neg already found - continue segmenting
foundword(X,Sem,Target), !,
            ( Target = no, Negstatus = X, !;
              Sem = neg, Negstatus = X, !;
              Sem \= neg, Target \= no, !
            );
```

```
true, ! % word is undefined
),
append(Start,[X],Beg), % part before segmentation
segment3(Rest,Newrest,Beg,Negstatus,Seg), !
% for finding type classes - parse as a sentence
whattoparse(Sem,P,Sent) :-
member(Sem,[cfinding,pfinding,morph,disease,device,proc,mproc,descriptor]),
    attemptparse(P,Sent,sentence,[Sem],impression,_).
% for bodyloc classes - parse as a bodyloc modifier
whattoparse(Sem,P,Sent) :-
    member(Sem,[bodyloc,region,side,position]),
    attemptparse(P,Sent,bodypart,_,_,_).
```

```
% file radrec.pl
% September 7, 1999
% fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [\+,not,once]).
                                   % same priority and type as \+
:- op(700, xfx, \{\=,\sim=\}). % same priority and type as = or ==
:- dynamic(domain/1).
                                 % domain being processed
:- dynamic(outputform/1).
                                 % form of output (needed to distinguish
                                 % markup of text from formatting forms
:- dynamic(currentsect/1).
                                 % section for outputting results
test genome (Outfile, Errfile, Unfile) :-
     get inputsents([], Toklist), !, % read in and tokenize input
     (Toklist = [], !, % error condition
      app_err1(_,Outfile,'No input sent'), !
      parse sentences (Toklist, Fmtlist, Failed, Undef, UnSent, impression,
bp,genome, , , 0),!,
      outputresults (Fmtlist, Failed, Errfile, Undef, Unfile, UnSent, Outfile,
                    full, line, genome, 1, 0, _, exe, plain)
     ).
outputresults (FmtlistO, Failed, Errfile, Undef, Unfile, UnSent, Outfile,
                Amount, Type, Exam, Compno, DocComp, NewCompno, Caller, Protocol) :-
      tell(Outfile),
     (Protocol = sgml, !, Op = sgml;
       Caller = server, !, Op = sgml;
        Op = plain),
      (Type = nested, !, % original output form - nested findings
        write('<nested>'), new line(Op),
         write(Fmtlist), new_line(Op), write('</nested>'),
         new line (Op), !
       ).
     (Caller = server,
      write_message(Unfile,Undef,Caller,'<undefined>','</undefined>')
      Caller = exe, Undef \= [],
      write_message(Unfile,Undef,Caller,'***** Undefined Words *****',[])
     %write_highlight([],UnSent,Caller)
      true
      ),
     (Caller = server,
     write('<noparse>'),!,
     write highlight (Undef, UnSent, Caller),
     write_highlight([],Failed,Caller), write('</noparse>')
     Caller = exe, Errfile \= [], Failed \= [],
     tell(Errfile),
     write('***** Sentences/Phrases Not Parsed *****'), nl,
     %write highlight(Undef, UnSent, Caller),
     write highlight([], Failed, Caller)
             % no Errfile to write to
     true
    ).
% set_args: Process options
```

```
% Argument options
% -p ProbFile (otherwise default is problem messages are not written to file)
% -i Infile (if input is supplied by file and not standard input
% -m Mode (default is bp; the 6 choices are bp, model - mode5)
% -o Outfile (if output should be file and not standard output)
% -? Provide list of default arguments
% -pr Protocol - sgml or plain (default is plain)
% -u Undefs (otherwise default is - undefined messages are not written
      to a file)
set args(Args, Mode, Infile, Outfile, Prbfile, Undef, Protocol) :-
      set mode(Args, Mode), set amount(Args, Amount),
      set protocol (Args, Protocol),
      set infile(Args, Infile), set outfile(Args, Outfile),
      set_prbfile(Args,Prbfile), set_undefs(Args,Undef).
set mode(Args, Mode) :-
    (nextto('-m',M,Args); nextto(m,M,Args)), !,
    modeis(M, Mode), !.
set_mode(_,bp). % default output type
modeis(relax, mode2) :- !.
modeis(strict, model) :- !.
modeis(skip, mode4) :- !.
modeis(longest, mode3) :- !.
modeis(best,bp) :- !.
modeis(model, model) :- !.
modeis(mode2, mode2) :- !.
modeis(mode3, mode3) :- !.
modeis(mode4, mode4) :- !.
modeis(mode5, mode5) :- !.
set protocol(Args, Protocol) :-
    (nextto('-pr',Protocol,Args); nextto('pr',Protocol,Args)),
     member(Protocol, [sgml, plain]), !.
set_protocol(_,plain).
set undefs(Args,Undefs) :-
    nextto('-u',Undefs,Args); nextto(u,Undefs,Args) , !. % undef file option
set_undefs( ,[]). % default is no file of undefineds created
set_infile(Args,Infile) :-
    nonvar(Infile), !; % Infile is set already
    nextto('-i', Infile, Args), !;
    nextto(i, Infile, Args), !.
set_infile( ,user_input).
                           % default is standard input
set prbfile(Args, Prbfile) :-
    nextto('-p', Prbfile, Args), !; nextto(p, Prbfile, Args), !. % prob file option
set_prbfile(,[]). % default is no file of problems is created
set_outfile(Args,Outfile) :-
    nonvar(Outfile), !; % Outfile is already set
    nextto('-o',Outfile,Args), !; nextto(o,Outfile,Args), !. % outfile option
set_outfile(_,user_output). % default is standard output
new_line(sgml) :- write('<br>'), nl, !.
new_line(server) :- write('<br>'),nl, !.
new line(exe) :- nl.
```

```
new line(plain) :- nl. '
write_message(_,[],exe,_,_) :- !.
write_message([],_,exe,_,]) :- !.
write_message(_,[],plain,_,_) :- !.
write_message([],_,plain,_,_) :- !.
write message (File, Contents, Caller, Begmsg, Endmsg) :-
   ( member(Caller,[exe,plain]), tell(File), !
    true),
    write(Begmsg), new_line(Caller),
   (Contents = []; write_list(Contents,1), new_line(Caller)
   (Endmsg = [], !;
    write(Endmsg), !, new_line(Caller)
sentend([X|_],Caller) :-
   member(X,['.',';','?']), new_line(Caller), !.
gettargets([],[]) :- !.
gettargets([ignore|Rest], [ignore|Rest]) :-!. % possibly ignore info.
gettargets([W1|Rest],[T1|Trest]) :-
     foundword(W1,_,T1),
                            % target for W1
     gettargets (Rest, Trest), !.
gettargets(W,W). % not in lexicon
isneg(X) :-
    intersect(X, [no, negative, deny, 'rule out']).
writeoutsent([Word|Rest]) :-
 write(''''), write(Word), write(''''), !,
  (Word = '''', write(''''), !; true),
  (Rest \= [], write(','), !, writeoutsent(Rest), !;
   true), !.
```

```
* This file contains predicates associated with SGML tags
% nextTag(+L,Tag,-PreTag,-PostTag) is true if
윰
      L is the starting List
      Tag is an SGML tag; it could be a variable or instantiated already
웋
      PreTag is portion of L preceding Tag
욯
      PostTag is portion of L following Tag
¥
nextTag(L, Tag, PreTag, PostTag) :-
    append(PreTag,['<',Tag,'>'|PostTag],L).
% endTag(+L,+Tag,-Pre,-Post) is true if
      L is the starting list
ş
욯
      Tag is the SGML end tag
      Pre is the portion of L preceding the end of tag
ş
      Post is the portion of L following the end of tag
욯
endTag(L, Tag, Pre, Post) :-
    append([Pre,['<','/',Tag,'>'],Post],L).
% enclosedPart(+L,+Tag,-Enclosed) is true if
      L is the starting List; it is assumed that L is portion of some
      list that follows a begin tag - i.e. '<', Tag|L
윰
¥
      Tag is the SGML tag
      Enclosed is the portion of text enclosed in tag; not including
¥.
Ł
      end tag.
enc!osedPart(L, Tag, Enclosed, Post) :-
    endTag(L, Tag, Enclosed, Post).
```

```
% file useful.pl - lexical lookup and utility tools
:-unknown(_,fail).
:-dynamic(sentence/1).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=, -=]). % same priority and type as = or ==
% useful.pl February 21, 1992
% preprocess(+S,+Bs1,-U,-Sem3,+Mode): preprocesses sentence to
            bracket lexical phrases and remove words/phrases in
            special db of noise words (nosem in nsphrase.pl db)
욯
        S is original sentence
ş
        Bsl is preprocessed sentence
        U is list of undefined words in sentence
        Mode is mode of process - in skip mode undefined words are removed
          from preprocessed sentence
preprocess (SO, Bsl, U, Sem3, Mode) :-
                                       %cfnew
                           % if beginning is 'A)' ignore
 checkbeg(S0,S),
  checkphrase(S,S1,Sem1), % bracket all phrases in phrasal lexicon first
  checklist(S1,U1,Bs,Sem2,Mode), % check that all words are in lexicon, remove
  checklist(Bs,U,Bs1,Sem3,Mode). % check for phrases after non-sem are removed
 %append(Sem1, Sem2, Sem1),
% tappend(Seml, Sem3, Semlist),
  %union(U1,U2,U).
% found checks if word X is defined as a single word, or if X starts a defined
% phrase
foundword(X) :-
     wdef(X,_,_), !.
foundword(X) :-
      semw(X, _, _, _),!.
%definition from tagged input
foundword(X) :-
   phr(X,_,_,_), !.
foundword([X Rest]) :-
      Rest \= [],
    phrasal(X,_,[X|Rest],_), !.
% 3/99 added foundword to search the new semact.pl lexicon
% phrasal using semp was added to util.lp
% found/2 returns semantic cat. of word
foundword(X,Sem) :-
    wdef(X,Sem,_).
foundword(X,Sem) :-
      semw(X,Sem,_,_).
%definition from tagged input
foundword(X,Sem) :-
      phr(X, Sem, [], _).
foundword([X|Rest],Sem) :-
    phrasal(X,Sem,[X|Rest],_).
% found/3 returns semantic cat. and target form
foundword(X, Sem, Form) :-
    wdef(X,Sem,Form).
foundword(X,Sem,Form) :-
      semw(X, Sem, Form, _).
%definition from tagged input
foundword(X,Sem,Form,_) :-
      phr(X,Sem,[],Form).
foundword([X|Rest], Sem, Form) :-
```

```
phrasal (X, Sem, [X|Rest], Form).
%collectsem(+Word,-Sem): Sem is the list of semantic classes corresponding
   to Word
collectsem (Word, Sem) :-
    setof(X, foundword(Word, X), Sem).
% missing checks if a word present in a sentence is defined
missing(X) :-
    member(X,S),
     not foundword(X).
% checkbeg(+S0,-S) checks beginning of sentence; if it begins with a letter or
% number followed by a ')', that part is skipped
checkbeg((X,')'|Rest),Rest) :- !.
checkbeg(X,X).
% checks every word in a list to see if it is defined; creates
% a new list of words not defined, and a new list of sentence
% where phrases are bracketed.
checklist([],[],[],[],[],_).
% if X is a list it has already been identified as a phrase in phrasal lex
checklist([X|Rest],Undef,Newrest,Semlist,Mode) :-
     is list(X),
     check_no_sem([X|Rest],Rest1,_),
     checklist (Restl, Undef, Newrest, Semlist, Mode), !. %is phrase part of nosem
checklist([X|Rest],Undef, [X|Newrest],Semlist,Mode) :-
     %collectsem(X,Sem),
     is_list(X), X = [W1|Tail],
    phrasal(W1,Sem,X,_),
     checklist(Rest, Undef, Newrest, Sem2, Mode) , !,
     append([Sem],Sem2,Semlist).
checklist([without|Rest],Undef,Newrest,Semlist,Mode) :-
     checklist([with, no | Rest], Undef, Newrest, Semlist, Mode).
this problem has to be fixed in preprocessor
$ check for a number with a ',' - "11,200" and fix it
*checklist([X,',',Y|Rest],Undef,[N|Newrest],[number|Semlist],Mode) :-
     number(X), number(Y), N is X * 1000 + Y, !,
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
t check for a literal number
                               *cfnew
checklist([X|Rest],Undef,[X|Newrest],[number|Semlist],Mode) :-
     number(X) .
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
beginning of List is a prefix of a phrase that is a complete finding
checklist(List, Undef, [Phrase | Newrest], [cfinding | Semlist], Mode) :-
     check_sem_finding(List, Rest, Phrase),
     checklist(Rest, Undef, Newrest, Semlist, Mode) , !.
beginning of List is a prefix of a phrase that is in nosemantic lexicon
checklist(List, Undef, Newrest, Semlist, Mode) :-
     check no sem(List, Rest, Phrase),
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
$ beginning of List is a prefix of a phrase that is in phrasal lexicon
checklist(List, Undef, [Phrase | Newrest], Semlist, Mode) :-
     get longest sem(List, Rest, Phrase, Sem),
     checklist(Rest, Undef, Newrest, Sem2, Mode), !,
     append (Sem, Sem2, Semlist).
% beginning of List is a single word that is in semantic lexicon
checklist([X|Rest], Undef,[X|Newrest],Semlist,Mode):-
```

```
collectsem(X, Sem), !,
     %foundword(X,Sem), !,
     checklist(Rest, Undef, Newrest, Sem2, Mode), !,
     append (Sem, Sem2, Semlist).
% beginning of List is an undefined word
checklist([X|Rest], Undefs, Nrest, Semlist, Mode):-
     checklist (Rest, Undef, Newrest, Semlist, Mode),
     (member(X,Undef), !; Undefs = [X|Undef], !),
     (Mode = skip, !, Nrest = Newrest;
      Mode = bpskip, !, Nrest = Newrest;
      Nrest = [X|Newrest]), !.
% if beginning is a number followed by a . followed by a non number
% skip;
         %cfnew
checkphrase([X,.],[X,.],[]) :- !.
checkphrase([X,.,Z|Rest],Y,Semlist) :-
     number(X), not(number(Z)), checkphrase(Rest,Y,Semlist), !.
% beginning of List is a prefix of a phrase that is a complete finding
% or a phrase in phrasal lexicon
checkphrase(List, [Phrase|Newrest], Semlist) :-
     (check_sem_finding(List,Rest,Phrase), Sem = [cfinding];
      get longest sem(List, Rest, Phrase, Sem)
     ), !,
     %check sem(List,Rest,Phrase,Sem)), !,
     checkphrase(Rest, Newrest, Sem2) , !,
     append (Sem, Sem2, Semlist).
checkphrase([W|Rest],[W|Newrest],Semlist) :-
     checkphrase (Rest, Newrest, Semlist).
checkphrase([],[],[]).
check_sem_finding([W|Tail],Tail,W) :-
           W = [W1|Rest], % W is bracketed already
           sem finding sent(W1,W, ).
check sem finding([W|Tail], Sfinal, Phrase) :-
           sem finding sent (W, Phrase, ),
           begsublist (Phrase, [W[Tail], Sfinal), !.
sem_finding_sent(_,_,) :- fail.
% check_no_sem(+Sent,-Rest,-Phrase): removes Phrase from Sent resulting
     in Rest if Sent begins with a phrase in nosem (non-semantic list).
check_no_sem([W|Tail],Sfinal,Phrase) :-
           nosem(W,Phrase), %phrase beg. with W that should be removed
           begsublist (Phrase, [W|Tail], S1),
           remove_comma(S1,Sfinal), !. % remove "," if it is next
%get_longest_sem(+Sent,-Rest,-Phrase,-Sem): Phrase is longest phrase that is
% a prefix of Sent; Rest is remainder and Sem is list of semantic classes
get_longest_sem(Sent,Rest,Phrase,[Sem]) :-
        setof(X,check sem(Sent,X),L), % set of Phrases
                                       % Phrase with maximum length
        maxphrase(L,[],Phrase,0),
                                        % rest of sentence after Phrase
        append(Phrase, Rest, Sent),
        foundword (Phrase, Sem).
% check_sem(+Sent,-Rest,-Phrase,-Sem): checks if phrase beginning with
        Sent is in phrasal lexicon; Rest is the remainder of Sent after phrase
        Sem is the semantic class
æ
check sem([W|Tail],Rest,Phrase,Sem) :-
           phrasal(W, Sem, Phrase,_),
           begsublist (Phrase, [W|Tail], Rest).
```

```
% file util.pl
% fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=,-=]). % same priority and type as = or ==
:- dynamic(wfst/6).
:- dynamic(addstotal/1).
:- dynamic (paragno/1).
:- dynamic(sectno/1).
:- dynamic(phr/4).
% wfst(+Rule, +Number, +Res, +Fmt, +S0, +S): well-formed symbol table
       Rule is the name of rule; Number is the option number
       Res is s for success and f for failure
¥
       Fmt is the format (for successes); for failure Fmt is []
ķ
       SO is the sentence position at the start of Rule
       S is the sentence position when Rule has been completed
        add to wfst
addst(Rule, Number, Res, Fmt, SO, S) :-
   ( checkst(Rule, _, Res, Fmt, SO, S), % different rule produced same result
      assert (wfst (Rule, Number, i, Fmt, SO, S));
   assert (wfst (Rule, Number, Res, Fmt, SO, S))), !.
addst(_,_,_,_):- !. % always succeed
% checkst(+Rule, -Number, -Res, -Fmt, +S0, -S): checks to see if rule has been saved
       in wfst
ક
checkst(Rule, Number, Res, Fmt, S0, S) :-
   wfst (Rule, Number, Res, Fmt, SO, S).
% beglist(L,Y) - is Y the head of list L
beglist([X],Y):- X = Y,!.
% splice(+L1,-L2) : L1 is a list of lists; L2 is merged list
splice(L1,L2) :- append(L1,L2), !.
*splice([],[]) :- !.
*splice([[]],[]) :- !.
*splice([X],X) :- !.
tsplice([[]|L1],L2) :- splice(L1,L2),!.
%splice([[[]]|L1],L2) :- splice(L1,L2),!.
%splice([X[[]]],L) :- splice(X,L),!.
%splice([L1,L2],L3) :-
       append(L1, L2, L3), !.
%splice([X|L1],L2) :-
        splice(L1,L3),
ž
      append(X,L3,L2) , !.
*splicerel - works with relations which have Arg1,...,Argn.
            It splices a Splicelist in each arg of relation
splicerel(Finding,Splicelist,Spliced) :-
           splice(Splicelist, Spl),
            (Finding = [rel, X | Rest], spliceargs (Rest, Spl, Sp),
             %splice([[rel,X],Sp],Spliced),!;
```

```
append([rel,X],Sp,Spliced),!;
              $splice((Finding,Spl),Spliced) ).
              append(Finding, Sp1, Spliced)).
*spliceargs - Splices a list into each element of a list
spliceargs([],_,[]) :-!.
spliceargs([Arg1|Rest],Splicelist,Spliced) :-
           $splice([Arg1,Splicelist],Sarg1),
           append (Argl, Splicelist, Sargl),
           spliceargs (Rest, Splicelist, Srest),
           %splice([[Sarg1],Srest],Spliced).
           append([Sargl], Srest, Spliced).
list([],(]).
list([X|[]],X).
list([X|L1],L2) :- list(L1,L3),
                   append([X],L3,L2), !.
% strip(L1,L2) removes extra square brackets from L
strip([L],L).
% B is a suffix of A and C is the difference
difflist(A,B,C) :- append(C,B,A).
% S is a sublist at beg. of L if there is a list Rest, which when appended
    to S results in L.
begsublist(S,L,Rest) :- append(S,Rest,L), !.
% checks that first element in list S has semantic category in Semlist
firstword([W1|_],Semlist) :-
    atom(W1), wdef(W1,Sem,_), % semantic category
    member (Sem, Semlist).
firstword([W1|],Semlist) :-
    is_list(W1), phrasal(W1,Sem,_,_),
    member (Sem, Semlist).
% removes phrases from first arg that are in nsphrase - lexicon of non-sem.
phrases
remove_no_sem([],[]) :- !.
remove_no_sem([W|Tail],Sfinal) :-
           nosem(W,Phrase), %phrase beg. with W
           begsublist(Phrase,[W|Tail],S1), %remove from sentence
           remove_comma(S1,S2), %remove "," if it is next
           remove no sem(S2, Sfinal), !.
remove_no_sem({W|Tail},Sfinal) :-
          remove_no_sem(Tail,S1),
          append([W],S1,Sfinal) , !.
remove_comma({','|Tail},Tail).
remove comma(S,S).
% remove_sem(+Sent,-NewSent): Sent is the original sentence, NewSent is
     stripped of all phrases that are defined in lexicon
remove sem([],[]) :- !.
remove_sem(S,NewS) :-
    remove_sem(Rest, NewS), !.
remove_sem(S, NewS) :-
    check_no sem(S,Rest,_),
                             % phrase in sent. is in nosem list - remove it
    remove_sem(Rest, NewS), !.
remove_sem([X|Tail],[X|NewS]) :-
    remove_sem(Tail,NewS), !. % not a phrase, process rest
% remove_words(+Sent,-NewSent): Sent is the original sentence, NewSent
    is stripped of all words that are in lexicon
```

```
remove words([],[]) :- !.
remove_words([X|Rest],NewRest) :-
     ( (foundword(X); number(X)),
                                    % X is defined in lexicon
      remove_words(Rest, NewRest) ,!;
      remove_words(Rest, New), NewRest = [X|New], ! % X is not in lexicon
%maxphrase(+ListofPhrases,+Maxin,-MaxOut,InitMaxLen) is true if
   ListofPhrase is a list of multi-word phrases,
     Maxin is phrase with maximum words so far
     MaxOut is phrase with maximum length of phrases in ListofPhrases
      InitMaxLen is length of initial phrase which is of max. length
maxphrase([],Maxin,Maxin,_) :- !. % no more phrases - maximum is same as maxin
maxphrase([P|Rest], Maxin, Maxout, InitMaxLen) :-
    length(P,Len), % length of first phrase
     ( Len > InitMaxLen, !, maxphrase(Rest,P,Maxout,Len);
      Len < InitMaxLen, !, maxphrase(Rest, Maxin, Maxout, InitMaxLen)
% facclex(Sem, W, SO, S) :-
   outputform(htext), !, acclex1(Sem, W, SO, S).
acclex(Sem, W, SO, S) :-
  acclex2 (Sem, W, SO, S).
acclex(Sem, W, SO, S) :-
  acclexss (Sem, Syn, Target, Features, SO, S).
% check lexicon for word or phrase, Target form is original W
acclex1(p, [P,C], [W|Rest], Rest) :-
        is list(W),
        find sem phrase(p, [P,C], W).
acclex1(p,[P,C],[W|S],S) :- atom(W),
                            wdef(W,p,[P,C]).
acclex1(Sem, [W], [W|Rest], Rest) :-
        is_list(W), %if bracketed list, get Sem and Code from phrasal lexicon
        find_sem_phrase(Sem,_,W).
acclex1(Sem, W, [W|S],S):-
                          atom(W),
                           wdef(W,Sem,_).
% check lexicon for word or phrase, Target form is taken from lexicon
%acclex2(Sem, Code, [W|Rest], Rest) :=
         is_list(W), %if bracketed list, get Sem and Code from phrasal lexicon
g.
         find sem phrase (Sem, Code, W).
acclex2(Sem, Code, [W|S],S):- foundword(W, Sem, Code),
                                            nonvar (Code) .
                                                             % protect against
lex. error
% find a phrase [W|Tail] in lexicon that begins with W and has category Sem
find sem phrase (Sem, Code, [W|Tail]) :-
        phrasal(W, Sem, [W|Tail], Code), % phrase and code beg. with W
        nonvar (Code) .
% case where phrase is already bracketed, look up phrase
sem finding phrasel(Code, [W|Tail], Tail) :-
        is list(W), %phrase is bracketed
        find sem sent (Code, W),
         nonvar(Code). %protect against lexical error
% case where phrase is already bracketed, look up phrase
sem finding phrase2 (Code, [W|Tail], Tail) :-
        is list(W), %phrase is bracketed
```

```
find_sem_sent(Code, W),
          nonvar(Code). %protect against lexical error
% Phrasal succeeds if lexicon contains phrase
phrasal (W1, Sem, Phrase, Code) :-
       phrase(W1, Sem, Phrase, Code, ). %multi-word phrase in lexicon
% added March15, 1999
phrasal (W1, Sem, Phrase, Code) :-
            semp (W1, Sem, Phrase, Code, Features).
% lexical definition from marked up input
phrasal (W1, Sem, [W1 | Tail], Code) :-
            phr (W1, Sem, Tail, Code).
acclexss(Sem, Syn, Target, Features, [W|S],S):-
            atom(W),
            semw (W, Sem, Target, Features),
            synw(W, Synclass),
            member (Synclass, Syn).
acclexss(Sem, Syn, Target, Features, [W|S],S):-
            is_list(W),
            find_phrasess(W, Sem, Syn, Target, Features).
find_phrasess([W1|Tail], Sem, Syn, Target, Features):-
            semp(W1, Sem, [W1 | Tail], Target, Features),
            symp(W1, [W1|Tail], Symclass),
            member (Synclass, Syn).
% lexical definition of a complete finding
find_sem_sent(Code,[W|Tail)) :-
         sem_finding_sent(W,[W|Tail],Code).
listify(C,[C]):-
         atom(C), !.
listify(C,C) :-
          is_list(C), !.
% distributes left mods and right mods over list of findings creating
% list of lists of findings with mods
distributemods([],[],_,_,) :- !.
distributemods(Dist, [D1|Tail], Lmods, Rmods, Type) :-
        distributemods(Dist2, Tail, Lmods, Rmods, Type), %distributed for remainder
        mergemods (Lmods, Rmods, Allmods),
        frame(D, Type, D1, Allmods), %Type frame with mods
        append([D],Dist2,Dist).
                                    % Combine findings to get list of findings
fixconj - if Leftmods has [certainty,no], and Conj = or, change Conj to and.
        no A or B = no A and no B; 'denies A,B, or C' is similar.
fixconj(Leftmods,Conj,[rel,and]) :-
        (member([certainty,no],Leftmods); member([certainty,deny],Leftmods)),
        Conj = [rel, or].
fixconj(_,Conj,Conj).
         write_sentences/1 inputs a PROLOG list and prints out lines
         which which are English sentences. No wrapping is done.
write_sentences([]) :- !.
write_sentences([X]) :- write(X), nl. % special sentence - section name
write_sentences(['<',p,'/','>']) :-
     write(''), nl.
                          % paragraph mark
write_sentences([X|Rest]) :-
        upper_first([X|Rest],[U|Rest]),
```

```
write(U), % First letter of first word made upper case
        %write(X),
         (X = U, chkforpunct(U,Rest), !, write_terms(Rest); % no space needed
        write(' '), write_terms(Rest)
         write_sentence/2 inputs a PROLOG list and prints out an English
ķ
         sentence wrapped. Idlen is the starting position of the sentence
         in the output.
*
          uses libraries ctypes, basic, not
write_sentence([X|Rest],Idlen) :-
    upper_first([X|Rest], [U|Rest]),
    write(U),
    name (U, LU), length (LU, L),
    (U = X, chkforpunct(U, Rest), !, write_terms(Rest, L+Idlen);
     write(' '), write_terms(Rest, L+Idlen+1)
        write_list inputs a PROLOG list and prints out a sentence like list.
         wrapped. Idlen is the starting position of the list in the output.
write_list([X|Rest],Idlen) :-
    write(X),
    name (X, LU), length (LU, L),
   ( chkforpunct(X, Rest), write terms(Rest, L+Idlen), !;
     write(' '), write terms(Rest, L+Idlen+1)).
%write_list(+List,+Idlen,-Idlenout)
% write_list prints out a sentence like list with wrapping if necessary.
    List is the list to be printed
    Idlen is the column position at start
    Idlenout is the column position at end
write_list([],Len,Len) :- !.
write_list([X|Rest],Idlen,Idlenout) :-
    atomic(X), write(X),
    name (X,LU), length (LU,L),
    (L + Idlen > 74, nl, Idlen2 = 1, !;
    Idlen2 = L + Idlen, !
  (chkforpunct(X,Rest), write list(Rest,Idlen2,Idlenout), !;
    write(' '), write_list(Rest,L+Idlen2+1,Idlenout), !
   is_list(X), write_list(X,Idlen,Idlen2), write_list(Rest,Idlen2,Idlenout).
upper_first([X|Rest], [U|Rest]):-
     name (X, \{L|Z\}),
 (is_alpha(L), Up is L - 32, !; Up = L),
name(U,[Up[2]), !.
% write_terms/1 writes out a word followed by blank, except for punctuations.
write terms([]) :- !.
% case where X is end of sentence
write_terms([X|Rest]) :-
   (X = '.'; X = ';'), % last word of sentence
   write(X), nl, !, write sentences(Rest), !.
% case where X is interior of sentence
write_terms([X|Rest]) :-
    write(X),
     (chkforpunct(X,Rest), write_terms(Rest);
```

```
write(' '), write_terms(Rest)
% write_terms(List,Used): writes the terms in list and counts the number
        of columns used; starts new line if 75 columns have been used
write_terms([],_) :- !.
% at end of list
write_terms([.], _) :- write('.'), nl,!.
write_terms([;], _) :- write(';'), nl,!.
% X is a punctuation, don't add to final count
write_terms([X|R],Used) :-
  ( R = [], write(' '), write(X), '!;
    chkforpunct(X,R),
    write(X), write_terms(R,Used), !
% X is last word in sentence
write terms([X,.], Used):-
   name(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(.);
    Total > 75, nl, write(' '), write(X), write(.)),
   nl, !.
% X is last word in sentence
write_terms([X,;], Used):-
   name(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(';');
    Total > 75, nl, write(' '), write(X), write(.)),
   nl, !.
% X is followed by ','
write_terms({X,','|Rest}, Used):-
   name (X, List), length (List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(','),
    write terms (Rest, Total);
    Total > 75, nl, write(' '), write(X), write(','),
    New is Need - 1, write terms (Rest, New)),
% writes blank + name of X, used is length of name+1
write terms([X|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 1.
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write_terms(Rest, Total);</pre>
    Total > 75, nl, write(' '), write(X), write terms(Rest, Len)),!.
write_terms(['X''s'|Rest], Used):-
   name(X; List), length(List, Len),
   Need is Len + 3,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write("'s"),
    write_terms(Rest, Total);
    Total > 75, nl, write(X), write_terms(Rest, Len)),!.
% processes sentences in Infile; writes formats to Outfile
% sentences beginning with '%' are treated as comments
testsents(Infile,Outfile) :-
```

```
see (Infile), seen, see (Infile),
   tell(Outfile),
   readtests,
   see (Infile), seen, told.
% reads next sentence and processes it
readtests :-
   read in(X),
   (X = end of file, !;
    X = [eoff, '.'], !;
    X = \{ ', ' \}, !;
    preprocess (X, Bs, Undef, Semlist, skip),
   ( Undef = [],
    dosent(X,Bs,Semlist,Fmt,Message,impression,W,chestxray,strict,0),
    write_sentence(X,1), write(Bs), nl,
    write(Fmt), nl;
    Undef \= [], write_sentence(X,1), write(Bs), nl, write(Undef), nl),
                  % read next sentence
    readtests
   ) .
% Reads in all sentences from input file and creates one list of all sentences
get_inputsents(Prevlist, Toklist) :-
    read_in(X),
     (X = end_of_file, Toklist = Prevlist, !;
     X = [eoff, '.'], Toklist = Prevlist, !;
     X = [''], Toklist = Prevlist, !;
     (last('',X), append(Toklist,[''],X), !;
                                              %remove
      append(Prevlist, X, Newlist),
      get inputsents (Newlist, Toklist)
     )).
*get sentence(+A,-B,-C)
* Gets next sentence from input list containing all sentences read in
Don't end a sentence if "." is preceded by a number and followed by
* a number and unit measure - 1.25 cm, 1.5 cm, .5 cm
t or is followed by a "." which is part of abbreviation
$ get_sentence(A,B,C) - A is list of all sentences in report.
                     - B is list containing one sentence
                     - C is remainder excluding B
* sgml tag for multi-word phrase containing '.' that is not end of sentence
get sentence(['<',phr|Tail],Sentence,LRest) :-
       enclosedPart(Tail,phr,Between,Rem), & Between beg. part of open phr and
close tag of phr
     append([sem,=,'"',Sem,'"'],MoreAttributes,Between), %Sem is value of sem
attribute
     (MoreAttributes = ['>'|Phrase], TargetList = Phrase, !;
      MoreAttributes = [t,=,'"'|TargetPlus], % Target terms plus end of phr
      by actual phrase
     Phrase = [W1|Rest],
     append (Phrase, SRest, Sentence),
     concat atom(TargetList, Target),
     assert(phr(W1,Sem,Rest,Target)), % assert lex def according to input
       %Phrase = [W1|PRest],
       %abbrev(W1,[W1|PRest],Target,_),
       get_sentence(Rem, SRest, LRest), !.
```

```
% Ignore sentence starting with '%', get next sentence
get_sentence(['%','%'|Rest],Sent,Remainder) :-
     get_sentence(Rest,_,Rem),
     get_sentence(Rem, Sent, Remainder).
get_sentence([X,.,Y,Z|Rest],[X,.],[Y,Z|Rest]) :- % break up "140. 3+"
     number(X), number(Y), Z = '+', !. % Y belongs to '+' for new sentence
get_sentence([X,.,Y,Z|Rest],[N|SRest],LRest) :-
                                                       $ 1.5 cm
      number(X), number(Y),
      % (wdef(Z,unit,); Z = x),
      Z = '+', % break up "140. 3+"
      1.
      name(X,D1), name(.,D2), name(Y,D3), name('E+00',D4),
      append([D1,D2,D3,D4],D), name(N,D), % put number together
      get sentence([Z|Rest], SRest, LRest).
% common abbrev
get_sentence([X,.|Rest],[X|SRest],LRest) :-
                                                  % abbrev ending in "."
% list of common abbreviations seen in reports should not end sentence
   member(X, [vs,dr,cm,mg]), get_sentence(Rest, SRest, LRest), !.
% list of start of names in reports should not end sentence
                                                 % abbrev ending in "."
get_sentence([X,.|Rest],[X|SRest],LRest) :-
   member(X, [ms, mr, mrs, dr, st]),
   skipname(Rest, Rest0),
                            % skip name part
   get_sentence(Rest0, SRest, LRest), !.
% more known abbreviations
get sentence([W1|Rest], [Rep[SRest], LRest) :-
     abbrevchk([W1|Rest],_,Rem,Rep), % abbreviation
     get sentence (Rem, SRest, LRest), !.
% possible simple xml tag for new paragraph
get_sentence(['<',p,'/','>'|Rest],Sent,Rem) :- %skip paragraph marker
    get_sentence(Rest,Sent,Rem), !.
% xml tag for sentence '<s>'
get_sentence(['<',s,'>'|Tail],Sentence,Rest) :-
      enclosedPart(Tail,s,Sent,Rest),
       (last('.', Sent), Sentence = Sent, !;
                                              %already has '.'
      append(Sent,[.],Sentence)
       ), !.-
                     %add '.'
get_sentence([.|Rest],[.],Rest) :- !. %end of a sentence
get_sentence([; |Rest],[;],Rest) :- !.
% interior of sentence
get_sentence([X|Rest],[X|SRest],LRest) :-
                        get_sentence(Rest, SRest, LRest).
get_sentence([],[],[]). % no more sentences
% abbrevchk(+WordList,-AbList,-RemList,-Target) is true if an abbrev is prefix
    of WordList, RemList is suffix of WordList (excluding prefix),
    AbList is prefix consisting of abbreviation
    and Target is target form of abbreviation
abbrevchk([W1|Rest], AbList, RemList, Target) :-
     abbrev(W1,AbList,Target,Dom), % abbrev knowledge base indexed by 1st word append(AbList,Rem,[W1|Rest]), % remainder of abbrev. must be in sentence
     (Dom = general, !; % abbrev. applies to all domains
      domain(Thisrep), Dom = Thisrep, !; % abbrev. applies to this domain
      is list(Dom), member(Thisrep, Dom) % this domain in abbrev. list
     ( % add back '.' to sentence if it also signals end of sentence
       Rem = [], last('.',AbList), RemList = ['.'], ! *no more words
      ; % words that generally start a new sentence
```

```
Rem = [W2]_], last('.', AbList), member(W2, [his,her,he,she,the,this]),
         RemList = ['.'|Rem], !
         ; % don't add '. back
       RemList = Rem
     ).
% skipname(+Beglist,-Endlist): skips next word after "mr" or "st"
skipname([],[]) :-!.
skipname([_,'''',s|Rest],Rest):- !. % "Luke's"
skipname([0,'''', |Rest],Rest):- !. % "O'Grady
skipname([ |Rest], Rest) :- !.
%get section(+Toklist, -Sents, -Rest, -Section, -Printname, Addno)
% Toklist contains input list; 1st sentence should be a header;
* Sents are all sentences in section; Section is name of section
& Sentences at beg. of Toklist are ignored until a section header is found
get_section([T|Toklist], Sents, Rest, Section, Printname, Addno) :-
       % first sentence should be section header
      get_sentence([T|Toklist],Sentence,RToklist),
      (section_header(Sentence, Rsent, Section, Printname), % Sentence is a section
       append (Rsent, RToklist, RToklist2),
       get_sectionsents(RToklist2,Sents,Rest),
       (Addno = 0, !; % testing if input begins with section header
       Addno = 1, ! , sectno(Sectno), Newno is Sectno + 1,
       retractall(sectno(_)), assert(sectno(Newno))
       retractall(paragno(_)), assert(paragno(1)), %lst parag. of section
       ; % 1st sentence is not a legitimate header - return []
       Section = []
       % get section(RToklist, Sents, Rest, Section) % skip till find header
     ~), !.
get_section([],[],[],[],_,_).
get_sectionsents([],[],[]) :-!.
get_sectionsents(Toklist,Slist,Rest) :-
     get_sentence(Toklist,Sentence,RToklist), % one sentence
     (\+ section_header(Sentence,_,_,), %more sentences in section
       get sectionsents (RToklist, RSents, Rest),
        append(Sentence, RSents, Slist)
       ; % the next section is a section header - return
     Rest = Toklist, Slist = []).
section_header(S,RestS,'report clinical information item',
          'CLINICAL INFORMATION: .') :-
    (S = [clinical,information,':','.'], !, RestS = [];
    begsublist([clinical,information,':'],S,RestS), !;
     S = [clininfo,':','.'], RestS = [], !;
    begsublist([clininfo,':'],S,RestS), !
   ).
section_header(S,RestS,'report impression item',
           'IMPRESSION: . ') :-
   (S = [impression, ':', .], RestS = [], !;
   begsublist([impression,':'],S,RestS), !
section_header(S,Rest,'report summary item','SUMMARY:.') :-
   S = [summary, ': | Rest].
```

```
section_header(S,RestS,'report description item','DESCRIPTION:.') :-
   (S = [description, ':', .], RestS = [], !;
    begsublist([description,':'],S,RestS), !
   ) .
section_header(S,Rest,'report diagnosis item','DISCHARGE DIAGNOSIS:.') :-
   (S = {discharge, diagnosis, ':' | Rest);
    S = [final,diagnosis,':'|Rest];
    S = [principle, diagnosis, ':'|Rest]; S = [associated, diagnosis, ':'|Rest];
    S = [transfer,diagnosis,':'|Rest];
    S = [diagnosis, '(', es, ')', ': '[Rest];
    S = [diagnosis,:|Rest]
  ), !.
section_header(S,Rest,'report laboratory data item','LAB DATA:.') :-
    S = {laboratory, data, ': 'Rest}, !.
section_header(S, Rest, 'report medications item', 'MEDICATIONS:.') :-
    S = [medications, ': '| Rest], !.
section_header(S,Rest,'report current medications item','MEDICATIONS:.') :-
    S = [current, medications, ': ' | Rest], !.
section_header($,Rest,'report discharge medications item',
        'DISCHARGE MEDICATIONS:.') :-
    S = [discharge, medications, ': '[Rest], !.
section_header(S,Rest,'report discharge disposition item',
     'DISCHARGE DISPOSITION: .') :-
    S = [discharge, disposition, ': '|Rest], !.
section_header(S,Rest,'report medications on admission item',
     'MEDICATIONS: . ') :-
    S = [medications, on, admission, ': '|Rest], !.
section_header(S,Rest,'report medications on transfer iterm',
     'MEDICATIONS:.') :-
     S = [medications, on, transfer, ': '|Rest], !.
section_header(S,Rest,'report procedure item','PROCEDURE:.') :-
  (S = [operation, ': '|Rest]; S = [procedure, ': '|Rest]
section_header(S,Rest,'report indications for procedure item','INDICATIONS:.')
  (S = [indications, for, procedure, ': '|Rest]; S =
[indications, for, operation, ': '| Rest]
 ),
  !.
section_header(S,Rest,'report preoperative diagnosis item','PREOP DIAGNOSIS:.')
   S = [preoperative, diagnosis, ': '| Rest], !.
section_header(S,Rest,'report admitting diagnosis item','ADMITTING
DIAGNOSIS: . '):-
   S = [admitting, diagnosis, ': '|Rest], !.
section_header(S,Rest,'report postoperative diagnosis item','DIAGNOSIS:.') :-
   S = [postoperative, diagnosis, ': '[Rest], !.
section_header(S,Rest,'report physical examination item',
        'PHYSICAL EXAM: . ') :-
   S = [physical, examination, ': '| Rest], !.
section_header(S,Rest,'report chief complaint item','CHIEF COMPLAINT:.') :-
   S = [chief,complaint,':'|Rest], !.
section_header(S,Rest,'report hospital course item','HOSPITAL COURSE:.') :-
   S = [hospital, course, ': '|Rest], !.
```

```
section header(S, Rest, 'report allergy item', 'ALLERGIES:.') :-
   S = [allergies, ': '|Rest], !.
section header(S, Rest, 'report follow up item', 'FOLLOW UP:.') :-
   S = [follow, up, ': '|Rest], !.
section_header(S,Rest,'report findings item','FINDINGS:.') :-
   S = (findings,':'|Rest], !.
section_header(S,Rest,'report indications and findings item','FINDINGS:.') :-
   S = [indications, and, findings, ': 'Rest], !.
section_header(S,Rest,'report indications and findings item','INDICATIONS:.') :-
   S = [indications, ': '|Rest], !.
section_header(S,Rest,'report provisional diagnosis item','PRELIM DIAGNOSIS:.')
   S = [provisional, diagnosis, ': '|Rest], !.
section_header(S,Rest,'report review of systems item','REVIEW OF SYSTEMS:.') :-
   S = [review, of, systems, ':'|Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [past, history, section, ': '[Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [past, medical, history, ': '|Rest], !.
section_header(S,Rest,'report social history item','SOCIAL HISTORY:.') :-
   S = [social, history, ': '| Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
 S = [history, ':'|Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [brief, history, ': '| Rest], !.
section_header(S,Rest,'report history of present illness item',
         'HISTORY OF PRESENT ILLNESS:.') :-
   S = [history, of, present, illness, ': '|Rest], !.
section_header(S,Rest,'report history of present illness item',
         'HISTORY OF PRESENT ILLNESS:.') :-
   S = [history, of, the, present, illness, ':'|Rest], !.
section_header(S,Rest,'report specimen item','SPECIMEN') :-
   S = [specimen|Rest], !.
% sentence consists of id number only or "." only.
isidentifier([X,.]) :-
        integer(X).
isidentifier([X,;]) :-
        integer(X).
isidentifier([.]) :- !. % sentence consists only of .
isidentifier(['.','<eos>']) :- !.
isidentifier(['<',p,'/','>']) :- % paragraph marker sentence - update no.
       paragno(N),
       retractall(paragno()),
       Newno is N + 1,
       assert (paragno (Newno)),
       retractall(sentno(_)),
       assert(sentno(0)).
% skipsentence is true, if sentence should be ignored.
% Skip sentences containing family info
skipsentence([X|_]) :-
```

foundword(X, family), !.

foundword(X,insurance), !.
% This occurs if sentence contains

skipsentence({X|}) :-

```
* a sequence in skips database and sentence also contains findings.
skipsentence([X|Rest], Semlist, Error) :-
                     % X is the beg. of subseq. in skip database
   skips([X|Sseq]),
   prefix([X|Rest],[X|Sseq]), % sentence contains subseq.
   (subtype(_,Semlist), % sentence contains information to be extracted
   Error = no; % don't try to segment
    Error = yes), !. % treat sentence as error and try to segment.
skipsentence([ |Rest], Semlist, Error) :-
   skipsentence (Rest, Semlist, Error).
% findingseg(+S,-Fseg,-Begseg): partitions sentence
        S is the sentence; Begseg is the segment preceding the
ş.
          modifiers of the finding; Fseg is the segment of S starting
욯
          with the leftmost modifier of the finding and consists of the
ક્ર
          remaining sentence.
findingseg(S,Fseg,Begseg) :-
    partition(S, Begpart, Restpart),
    (Begpart = [], Begseg = [];
    Restpart = [], Fseg = [], Begseg = S;
    right1stmod(Begpart, Begseg, Modseg)),
    append (Modseg, Restpart, Fseg).
findingseg(_,[],_) :- !.
actionfindingseg(S,Fseg,Begseg):-
      partition(S, Begpart, Restpart),
    (Begpart = [], Begseg = [];
     Restpart = [], Fseg = [], Begseg = S;
      reverse (Begpart, ReversedBefore),
          findsubstance (ReversedBefore, Rest),
          append (Substancepart, Rest, ReversedBefore),
          reverse (Substancepart, Leftpart),
        reverse (Rest, Begseg),
      append(Leftpart, Restpart, Fseg)).
actionfindingseg(_,[],_) :- !.
findsubstance([],[]):-!.
findsubstance([X|Rest],Rest):-
      substance( ,[X],[]),!.
findsubstance([X Rest1], Rest):-
      findsubstance (Rest1, Rest).
% partition(+S,-Begpart,-Restpart): partitions sentence
        S is initial
% partition(+S,-Begpart,-Restpart): partitions sentence
        S is initial sentence; Begpart is part of sentence before the
          finding; Restpart is the rest of the sentence and starts with
ð.
          the finding. If there are 2 consecutive findings
*
          the 1st one is considered a modifier
partition([],[],[]) :- !.
partition([X|Rest],[X|Begpart],Restpart) :-
    not(isfinding(X)), !, partition(Rest, Begpart, Restpart).
partition([X,Y|Rest],[X],[Y|Rest]) :-
    isfinding(X), isfinding(Y), !.
partition([X|Rest],[],[X|Rest]) :-
    isfinding(X), !.
% isfinding(+X): is true if X is a word or phrase whose semantic class
        is a finding or subtype of finding.
```

```
isfinding(X) :-
                        % semantic class of word
     foundword(X,Sem),
                         % is class a type of finding, recommend, or technique
     subtype(_, [Sem]).
% semantic class which are types of relevant information
subtype(finding,Sem) :-
     intersect(Sem, [attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, promote,
      signal]).
% there is only one type of technique class
subtype(technique, Sem) :-
     member (technique, Sem).
subtype(time, Sem) :-
     intersect(Sem,[status,sstatus,change,tmper,vstatus]).
findinginlist (Sem) :-
    intersect(Sem, (attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, promote,
      signal]).
% chkforpunct(+W, +Rest): is true if there should be no space after word W
chkforpunct(W, _) :- member(W, ['/', '<', '>', '-', '"', '[', ']',
               `!{';'}','<u>_</u>','+','=','|','\']), !.
% nothing left to write.
chkforpunct(W,[]) :-!.
% is true if there should be no space before word after current word
chkforpunct(_,[W|_]) :-
   ispunct(W).
% ispunct(+W) is true if W is a punctuation for sentence print out
% The following characters are not treated as punct: ~ ^* # $ ^* & *
ispunct(W) :- member(W,[',',',',',',',',',',','?','?',''','-',':','"','[',']',
               '{','}','(',')','_','+','=','|','\','%','@']).
% rightlstmod(List, Firstpart, Modpart): Modpart begins with the first
    word in List which is a modifier; Firstpart are the preceding words
right1stmod([],[],[]) :- !.
% X is a modifier or finding; Beginning part is empty
rightlstmod([X|Rest],[],[X|Rest]) :-
   foundword (X, Sem, Target),
   (modifier(Sem); Sem = p, Target = [_,conn]; subtype(_,[Sem])), !.
% X is not a modifier or finding
right1stmod([X]Rest],[X]Firstpart],Modpart) :-
   right1stmod(Rest, Firstpart, Modpart).
% frame(Frame, Type, Value, Mods): creates a list Frame, whose lst
        element is Type, 2nd element is Value, and 3rd is a list of
ક
        modifier frames or is emtpy
% Case where modifier list is empty; Value should be atom except for
% certain types;
frame([Type, Value], Type, Value, X) :-
    (X = {]; X = {[]}}),
    atom(Value), !.
% Special cases where value of type should be a list
frame([Type,[H|R]],Type,[H|R],X) :-
       (X = []; X = [[]]),
       oklist(Type), !.
% Modifier list is merged with list consisting of Type and Value
frame (Frame, Type, Value, Mods) :-
     atom(Value),
     append([Type, Value], Mods, Frame), !.
```

```
frame (Frame, Type, [H|R], Mods):-
     is list(R),
     append(R, Mods, NewMods),
     append([Type, H], NewMods, Frame), !.
% Components of Frame
frame([Type, Value | Mods], Type, Value, Mods) :- !.
% Value of Type should not be a list; first element of value is real value
frame([Type, H, Rest], Type, [H|Rest], []) :- !.
% Special cases where value of type should be a list
frame([Type, [H|R]], Type, [H|R], []) :- 
    oklist(Type), !.
% Value of Type should not be a list; first element of value is real value
frame (Frame, Type, [H | Rest], Mods) :-
    mergemods (Rest, Mods, NewMods),
    append ([Type, H], NewMods, Frame).
% mergemodinf(-F,+Frame,+Mods): Frame is a type-value-mod frame; Mods
    is an additional set of modifiers for Frame; mergemodinf adds Mods
    to Frame, resulting in F.
mergemodinf([],[],_):-!.
mergemodinf(F, [rel, X | Rest], Modrel):-
        mergemodinf(F1, Rest, Modrel),
        append([rel,X],F1,F),!.
mergemodinf(F, [F1, X | Modfin], Modrel):-
        atom(F1), mergemods(Modrel, Modfin, Mod),
        append([F1,X],Mod,F),!.
mergemodinf(F,[H|R],Modrel):-
       mergemodinf(F1,H,Modrel),
        mergemodinf(F2,R,Modrel),
        append([F1],F2,F).
% addmodstof(+Args,+Mods,-NewArgs) is true if Args is a list of formats,
% Mods is a list of modifiers and NewArgs is a list of formats where Mods
% has been added to modifier list of that format
addmodstof([],_,[]) :- !. % no more formats
addmodstof([Format1|Rest], Mods, [F1|NewRest]) :-
       mergemodinf(F1,Format1,Mods), % merge modifiers into 1st format
       addmodstof(Rest, Mods, NewRest), !. %add modifier to remaining
% oklist(+Type): is true if Type can have a list as its value
oklist (unitval).
oklist (age).
oklist (measure).
oklist(prev timeunit).
oklist (future exam).
% mergemods(+Mods1,+Mods2,-Mod): Mods1 and Mods2 are a list of modifier lists
        Mod is the merged list; some elements of Mods1 and Mods2 may be
¥
        empty
mergemods([],M,M) :- !.
mergemods (M, [], M).
mergemods (Mods1, Mods2, Mod) :-
        delete (Mods1, [], M1),
        delete (Mods2, (), M2),
        append (M1, M2, Mod).
* addmod(+Mod,+Modlist,-NewMod): NewMod is formed by including
        Mod into Modlist
addmod([],Mod,Mod):-!.
```

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addmod(Mod,[],[Mod]) :- !.
addmod(Mod, Modlist, NewMod) :-
   append([Mod],Modlist,NewMod).
% modlist(+ListofMods,-Mods): ListofMods is a list consisting of
    individual modifier frames, some of which may be empty
    Mods is formed as a list of non-empty modifiers
modlist([],[]) :- !.
% ignore a modifier which is an empty list
modlist([[]|R], Mods) :-
    modlist(R, Mods), !.
modlist([[H|R1]|R2],Mods) :-
    atom(H), !,
    modlist (R2, Rmods),
    addmod([H|R1], Rmods, Mods).
modlist([[H|R1]|R2],Mods) :-
    is list(H), !, % is first element is a list
    modlist (R2, Rmods),
    mergemods([H|R1],Rmods,Mods).
$bpframe: creates from for sequences of bodyloc/region/position
bpframe(F,[],_,F,[]):- !. % only 1 bodyloc
bpframe(F,[], Type, Bp1, Bp2) :- % no conj relation but more than 1 bodyloc
        frame(Bp1,Bp1Type,Bp1Val,Bp1Mods), %contents of Bp1 frame
        frame (Bp2, Bp2Type, Bp2Val, Bp2Mods), %contents of Bp2 frame
        ( (BplType = region; BplType = position),
         Bp2Type = bodyloc, % 'left lung', 'area of lung'
         mergemods(Bp1Mods,Bp2Mods,BpMods), %new region modifier
         frame(NewBp2Mods, BplType, Bp1Val, BpMods), %new Bpl frame w new mod
         BplType = bodyloc, Bp2Type = bodyloc, Type = main, %Bp2 is main
         mergemods(Bp1Mods,Bp2Mods,BpMods), %new bodyloc modifier
         frame (NewBp2Mods, Bp1Type, Bp1Val, BpMods), % 'joint of shoulder'
                                                  % main bp frame is shoulder
         frame(F, Bp2Type, Bp2Val, [NewBp2Mods])
         mergemods (Bp1Mods, Bp2Mods, BpMods),
         frame(NewBp1Mods,Bp2Type,Bp2Val,BpMods), % 'shoulder joint'
         frame(F,BplType,BplVal,[NewBplMods])
                                                   % main bp frame is shoulder
bpframe(F,Rel,_,Bp1,Bp2) :- % no conj relation but more than 1 bodyloc
        Rel = [rel,Conj|_], Bp2 \= [],
        mergemods([Bp1],[Bp2],Conjargs),
        frame(F,rel,Conj,Conjargs).
getrelation(R,F1,F2,F) :-
        (F2 = [],
            (F1 = [rel,Conj1|Rest1], R = [rel,Conj],
                                   (Conj1 = ','; Conj1 = or; Conj1 = and),
                                   (Conj = ','; Conj = or; Conj = and);
              Rest1 = \{F1\}),
            (F2 = [rel,Conj2|Rest2],
                                   (Conj2 = ','; Conj2 = or; Conj2 = and);
              Rest2 = [F2]),
            %splice([R,Rest1,Rest2],F);
            append([R,Rest1,Rest2],F);
          F2 = [], F = F1 ).
```

uptotal : addstotal(X),
 X =< 50,
 NewX is X + 1,
 retractall(addstotal(X)),
 assert(addstotal(NewX)), !.</pre>

Appendix F

```
$save{'a'}='AAAC';
 $save{'b'}='AAAG';
 $save{'c'}='AAAT';
 $save{'d'}='AACC';
 Ssave{'e'}='AACG';
 $save{'f'}='AACT';
 $save{'g'}='AAGC';
 $save{'h'}='AAGG';
 $save{'i'}='AAGT';
 $save{'j'}='AATC';
 $save{'k'}='AATG';
- $save{'1'}='AATT';
 $save{'m'} = 'ACAC';
 $save{ 'n '} = 'ACAG';
 $save{'o'}='ACAT';
 $save{ 'p' } = 'ACCC';
 $save{'q'}='ACCG';
 $save{'r'}='ACCT';
 $save{'s'}='ACGC';
 $sa 'e{ 't' } = 'ACGG';
 $save{'u'}='ACGT';
 $save{'v'}='ACTC';
 $save{'w'}='ACTG';
 $save{'x'}='ACTT';
 $save{'y'}='AGAG';
 $save{ 'z'} = 'AGAT';
 $save{'0'}='AGCC';
 $save{'1'}='AGCG';
 $save{'2'}='AGCT';
 $save{'3'}='AGGC';
 $save{'4'}='AGGG';
 $save{ '5'} = 'AGGT';
 $save{'6'}='AGTC';
 $save{'7'}='AGTG';
 $save{'8'}='AGTT';
 $save{'9'}='ATAT';
 $save{' '}='ATCC';
 $save{'}'}='ATCC';
 $save{'{'}='ATCC';
 $save{';'}='ATCC';
 $save{':'}='ATCC';
 $save{'"'}='ATCC';
 $save{'\''}='ATTC';
 $save{'?'}='ATCC';
 $save{'!'}='ATCC';
 $save{'#'}='CCCG';
 $save{'$'}='CCCT';
 $save{'^'}='CCGG';
 $save{'&'}='CCGT';
 $save{'*'}='CCTG';
 $save{'('}='ATCC';
 $save{')'}='ATCC';
```

NXQ2:257372.1



```
$save{'_'}='CGCT';
$save{'-'}='ATCC';
$save{'+'}='CGGT';
$save{'='}='CGTG';
$save{'}'}='CGTT';
$save{'{'}='CTCT';
$save{','}='ATCC';
$save{'.'}='ATCC';
$save{'|'}='CTTG';
$save{'%'}='CTTT';
$save{'/'}='ATCC';
$save{'\\'}='GGTT'; .
$save{ '@'} = 'GTGT';
$save{"\n"}='ATCC';
$save{'<'}='GTTT';
$save{'>'}='GTTT';
$save{'~'}='GTTT';
```



Appendix F

```
#!/usr/bin/perl
#Scan.pl : Scans blast output
#Author: Michael Krauthammer
#Copyright: c.1999, Columbia University
#Variables
#blast input/file
$input file="genebank.result";
#program output
$output_file="match.txt";
#open datastream for file which contains blast output
    open (INPUT,'/storage/psi-blast/MarkIt/programs/markIt.result');
while ($line=<INPUT>) {
    if ($line=-/\>gi\|(\d*) (.*)\,(.*)\,(.*)/){
   $target=$4;
   $gi =$1;
   $semantic_class=$3;
   }
   if(sline=-/Length = (.*)/){
   $lengthI=$1;
    if \{\text{line=} \sim | \text{Identities} = (\d^*) \)
   $length_actual=$1
    if ($line=~/Query: (\d*)/){
   $start=$1;
    }
#print if Subj 1, sometimes match 2 or 3 line long
    if ($line=-/Sbjct: 1 /) {
   if (($length_actual/$lengthI) > .9){
$target,"|",$start,"|",$start+$lengthI,"|",$semantic_class,"|",$gi,"\n";
```



Appendix

```
#!/usr/bin/perl
 #nucleotide_text_parser.pl
#Author: Michael Krauthammer, c.1999 Columbia University
open (INPUT, $ARGV[0]);
 #read uncoded input text line by line (chop it)
 $all='';
while ($line=<INPUT>) {
     $all=$all.$line;
open (INPUTII,'/storage/psi-blast/MarkIt/programs/markItII.result');
open (OUTPUT, '>result.txt');
 #first part: check matches, store positions
 while ($line=<INPUTII>) {
(\text{name}, \text{start}, \text{end}, \text{semantic}_{class}, \text{gi}) = \text{line} = -/(.*) \setminus |(.*) \setminus |(.*) \setminus |(.*) \setminus |(.*) |
 #divide by 4 (4 letter code)
 $start=($start-1)/4;
 Send= (Send-1) /4;
 #get substring
 if ($start != 0){
 $letters=substr($all,$start-1,$end-$start+3)."|";
 } else {
 $letters = ' '.substr($all,0,$end+2)."|";
 ($letter_beginning)=$letters=-/(^.)/;
 $letter end=substr($all,$end,1);
 $letter_endII=substr($all,$end,2);
 #ignore matches that are in the MIDDLE of sentences, allow plurals
 $letter beginning=~tr/[A-2]/[a-z]/;
 $letter end=-tr/[A-Z]/[a-z]/;
 if ((!($letter_beginning=~/[a-z]/)) && ((!($letter end=~/[a-z]/)) ||
 ($letter endII=~/s /))){
 #make sure only the first occurence is stored at this position
    if ($save{$start}==''){
    $save{$start}=$end.'|'.$semantic class.'|'.$gi;
           foreach $key(keys(%save)){
     ($end_key) = $save{$key}=-/^(.*)\\/;
     if ($end key>$end) {
        if ($key<$start){
           $save{$start}='null',
     }
```

```
#second part: print out marked up document
sort(%save);
for ($i=0;$i<length($all);$i++){
    if ((!$save{$i}=='null') && ($save{$i}==/./)){
        ($end,$semantic_class)=$save{$i}==/(.*)\\(.*)\\/;
        print OUTPUT '<phr="',$semantic_class,'">';
        $store=substr($all,$i,$end-$i);
        print OUTPUT $store;
        print OUTPUT "</phr>";
        $i=$end-1;
        } else {
        $store=substr($all,$i,1);
        print OUTPUT $store;
}
```

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98	-178	-6665	398	-178	-3889	1349	-178	-3377	-651	-178	-3303	753	-178	-8533	-617	-178	-8533	487	-178	-3481	-570	-178	-3247	148	-178	-8329	304	-178	-8333	1718	-178	-3795	-442	-178	-3274	-735	-178	8109	-740	-178	8111	831	-178
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-7114	413	919	-7114	413	979	-7114	452	919	-6968	461	979	-6963	460	979	-6945	460	979	-6945	460	919	-6945	484	979	-6836	558	979	-6490	558	979	-6490	263	979	-6486	263	979	-6486	568	979	-6484	612	616	-6237	612
-16	505	206	-16	1301	206	-130	750	206	-44	066	206	-44	1181	506	-18	418	206	-18	1183	206	-99	905	206	-259	1335	902	-24	1075	206	-39	1069	506	-24	292	206	-39	1863	506	-217	733	206	-29	1281
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1453 1398 -735 69 546 -1118 -1792 -14 1712 -2507 744 -676 772 -541 628 -585 -76 1118 -1712 -2507 744 -677 -164 41 -73 -335 -76 -112 -64 -130 -677 -164 41 -73 -335 -76 -112 -64 -130 -677 -164 41 -73 -335 -76 -137 -136 -37 -64 -3001 519 343 984 591 68 -334 -416 -37 -164 41 -73 -335 -76 -137 -130 -130 -54 -30 -54 -30 -54 -30 -48 -130 -67 -164 41 -73 -335 -54 -37 -12 -12 -132 -312 -365 -635 -635 -635 -635 -635 -635 -635 -635		,	•	7	.732	-1329	•	- 206	•	•											
206 979 178 352 36 372 585 -635 438 -130 -677 -164 41 -73 -335 -54 27 -12 -64 10497 -4549 -732 -1329 -3696 -116 • <td></td> <td>7 145</td> <td>٠</td> <td></td> <td>69</td> <td>546</td> <td>•</td> <td>-1792</td> <td>-14</td> <td>1712</td> <td>-2507</td> <td>744</td> <td>-676</td> <td>277</td> <td>-541</td> <td>628</td> <td>-585</td> <td>-76</td> <td>112</td> <td>-2632</td> <td>1084</td>		7 145	٠		69	546	•	-1792	-14	1712	-2507	744	-676	277	-541	628	-585	-76	112	-2632	1084
-64 · 10497 · 4549 · 732 · 1329 · 3696 · 116 · • · · · · · · · · · · · · · · · · ·		- 20			-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	.54	27	-12	-255	- 97
742 11346 1192 402 202 9 1740 3 1053 -964 -3001 519 343 984 591 68 -334 -416 206 979 -178 -352 -36 -635 438 -130 -677 -164 41 -73 -335 -54 27 -12 -32 -10434 -557 -132 -1329 -3837 -105 -139 -56 -208 -151 -154 -17 -135 -54 27 -12 206 979 -178 -132 -136 -696 -632 -635 438 -130 -677 -164 41 -73 -335 -54 27 -12 206 979 -178 -132 -136 -137 -144 -73 -154 41 -73 -335 -54 27 -12 100 -131 119 -690 -582 -146 <			•		. 732	-1329	-3696	-116	•	•											
206 979 -178 -352 -36 372 585 -635 418 -130 -677 -164 41 -73 -335 -54 27 -12 -32 -10434 -557 -732 -1329 -387 -105 -<		8 -74			402	202	σ	-1740	~	1053	- 964	-3001	519	343	984	591	68	-334	-416	-2580	9
- 12 - 10414 - 5577 - 712 - 1129 - 1187 - 105		. 20			-355	- 36	372	585	-635	438	-130	-617	-164	41	-73	-335	-54	27	-12	-255	-97
-639 746 237 -154 361 -696 1779 -1139 526 -2880 -1519 397 269 -320 -452 -2108 206 979 -178 -352 -36 375 -418 -130 -677 -164 41 -73 -335 -54 27 -20 -10404 -6555 -732 -1329 -3115 -164 • <t< td=""><td></td><td></td><td></td><td>-5577</td><td>-732</td><td>-1329</td><td>-3837</td><td>-105</td><td>•</td><td>•</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>				-5577	-732	-1329	-3837	-105	•	•											
206 979 -178 -352 -36 172 585 -635 438 -130 -677 -164 41 -73 -335 -54 27 -20 -10404 -6255 -732 -1329 -1315 -164 • • • • 9.0 -2440 1026 -717 1162 71 135 -926 -602 206 979 -178 -352 -184 -8 •<		9 -63			- 154	361	969-	1779	-1139	529	262	-2880	-1519	397	269	-320	-452	-2108	638	-2555	102
-20 -10404 -6255 -732 -1329 -3215 -164		. 20(.352	-36	372	585	-635	438	.130	-677	-164	41	-73	:335	-54	27	-12	-255	-97
100 -1331 119 -690 -582 -1437 -807 420 930 -2440 1026 -717 1162 71 157 -926 -602 206 979 -178 -352 -36 372 585 -635 438 -130 -677 -164 41 -73 -315 -54 27		2(.6255	. 732	-1329	-3215	-164	•	•					•						
206 979 .178 .352 .36 372 585 .635 438 -130 .677 .164 41 .73 .335 .54 27 .7 .126 .10416 .3591 .732 .1329 .2293 .194 .	-			119	069-	-582	.1437	-807	420	930	-2440	1026	-717	1162	1,	157	- 926	-602	455	1032	105
-126 -10416 -3591 -732 -1329 -2993 -194		- 206		.178	-352	-36	372	585	-635	438	-130	-677	- 164	41	- 73	-335	-54	27	.12	-255	-97
-284 ·1265 ·795 993 1079 ·1872 ·579 ·2879 557 ·468 ·2920 ·109 492 1099 ·355 ·1375 1068 206 979 ·178 ·352 ·36 372 585 ·635 438 ·130 ·677 ·164 41 ·73 ·335 ·54 27 ·29 ·10335 ·5734 ·732 ·1329 ·2662 ·248		126		.3591	-732	.1329	.2993	.194	•	•											
206 979 .178 .352 -36 372 585 -635 438 -130 -677 .164 41 -73 -335 -54 27 -29 -10335 -5734 -732 -1329 -2662 .248	-			- 795	993	1079	- 1872	-579	.2879	557	-468	-2920	-109	492	1099	-355	-1375	1068	115	-2499	-105
-29 -10335 -5734 -732 -1329 -2662 .248 • • • • • • • • • • • • • • • • • • •		- 206		.178	. 352	-36	372	585	-635	438	-130	-677	.164	41	.73	-335	-54	27	-12	-255	. 97
.617 923 1065 .28 958 .1917 95 .2381 679 .1864 .662 .1612 .721 1624 .240 .410 26			- 10	-5734	-732	.1329	-2662	.248	•	٠											
	-	•		1065	- 28	958	-1917	95	.2381	619	-1864		-1612	-721	1624	-240	-410	56	547	1088	- 75

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/10302

A. CLASSIFICATION OF SUBJECT MATTER									
IPC(7)									
US CL	US CL: 702/27; 706/45, 47; 712/200 According to International Patent Classification (IPC) or to both national classification and IPC								
	DS SEARCHED	iational classification and if C							
	Minimum documentation searched (classification system followed by classification symbols)								
	02/27; 706/45, 47; 712/200	by classification symbols,							
Documentation	on searched other than minimum documentation to the	e extent that such documents are include	d in the fields searched						
	ata base consulted during the international search (nanontinuation Sheet	ne of data base and, where practicable, s	search terms used)						
C. DOC	UMENTS CONSIDERED TO BE RELEVANT								
Category *	Citation of document, with indication, where ap	propriate, of the relevant passages	Relevant to claim No.						
Y	YUAN et al. Towards detection of orthologues in se 1998, Vol. 14, No. 3, pages 285-289, see entire doc		1-32						
Y	BAILEY, JR. et al. Analysis of EST-driven gene as Genome Research. 1998, Vol. 8, pages 362-376, see		1-32						
Y	SONNHAMMER et al. Pfam: A comprehensive database of protein domain families based on seed alignments. Proteins: Structure Function and Genetics. 1997, Vol. 28, pages 405-420, see entire document.								
	documents are listed in the continuation of Box C.	See patent family annex.							
"A" document	Special categories of cited documents: "T" Later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention								
-	cular relevance "X" document of particular relevance; the claimed invention cannot be application or patent published on or after the international filing date "X" document of particular relevance; the claimed invention cannot be considered no involve an inventive step								
establish	when the document is taken alone when the document is taken alone when the document is taken alone document of particular relevance; the claimed invention cannot be								
"O" document									
	published prior to the international filing date but later than the ate claimed	"&" document member of the same patent	family						
Date of the a	ctual completion of the international search	Date of mailing of the international sea	rch report						
	(05.06.2000)	U (JUL ZUUU	· 						
	ailing address of the ISA/US poissioner of Patents and Trademarks	Authorized officer	,						
Box	PCT	Young J. Kim							
	hington, D.C. 20231 D. (703) 305-3230	Telephone No. (703) 308-0196							
	Facsimile No. (703) 305-3230 Telephone No. (703) 308-0196								

Form PCT/ISA/210 (second sheet) (July 1998)

PCT/US00/10302
tinuation of B. FIELDS SEARCHED Item 3: STN Commercial Database (Biosis, Medline, Embase, Embal,
earch, Biotechds, Caplus) 2.0 (USPT, EPAB, JPAB, DWPI, TDBD)
ch Terms: gene tree, species tree, Hidden Markov, HMM, overlap, BLAST
PCT/ISA/210 (extra sheet) (July 1998)

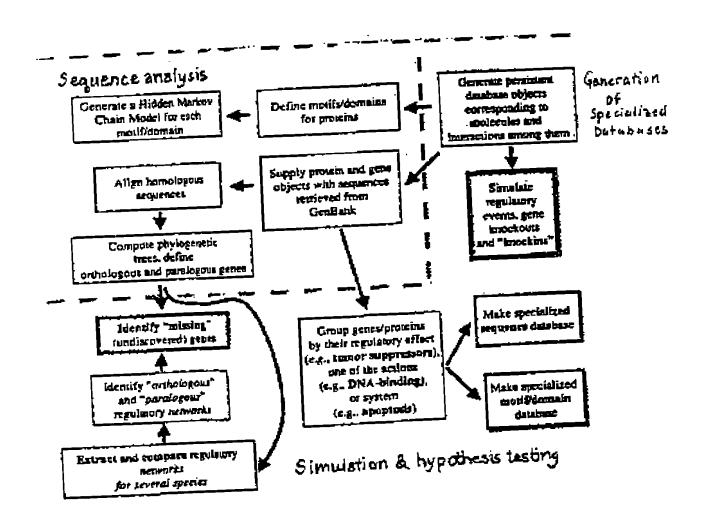


FIGURE 1

2/23

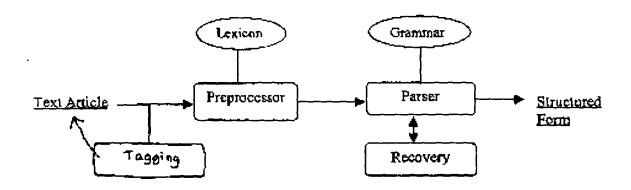


Figure 2

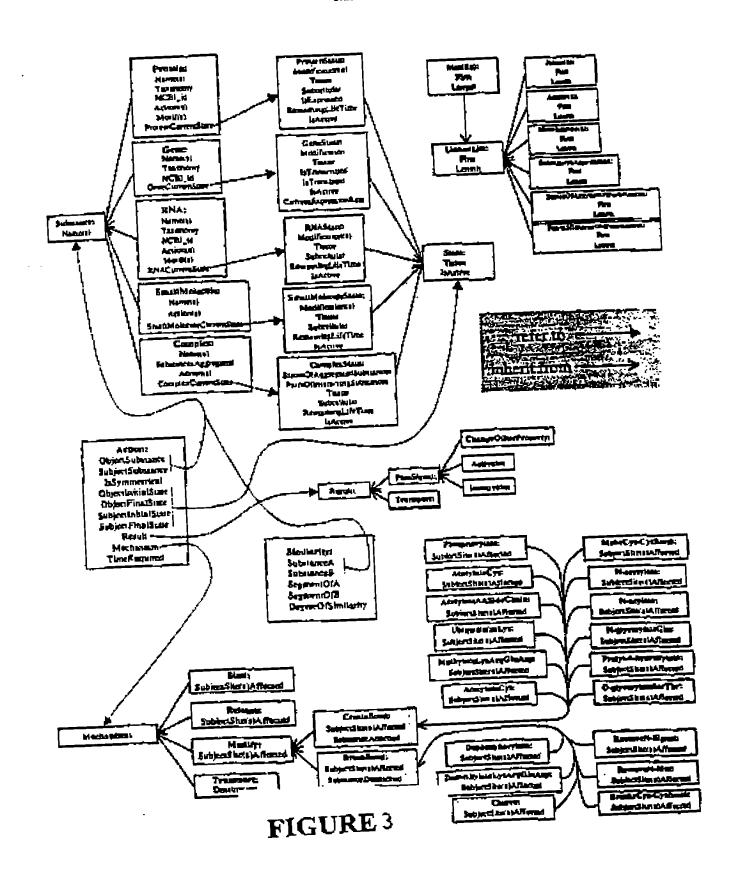


FIGURE 4

hd-sl/ bd / bd-ss/ bd-s/ Bax / Bb / Bak/ p21 / RGFLB / NIG / Nahl / Nar77 / Nor1 / Nor1 / RXR / galectic-1 / N-glyana / CRTF / ich / typ / ZAP-70 / rad / rad / MAP / protein bloom C / FEC / phosphotom relelements / NF-AT / AF / 148-3 / Rad-1 / Bd-s / Interiorition / IL-1 / EL-3 / typoidine / IGF-L / CDS / Apo-L / RIP / FAFT / PADD / FAF-L / TWUR / TRAP / EB19K / NBk / Mch2 / CP93 / ICE / FLICE / Nadc-2 / TK / Mch3 / Mch4 / ICE-1s / mar-1 / INAm3 / trapms / MACH1 / Mch5 / apopula / Yapm / ECH / CME / cmi-3 / cmi-4 / mch3 / Mch2 / McKE / McKE / McKE / McKA / TAG-1 / Sec / FAST / p33 / p42 / ERX2 / P44 / ERX2 / SAPE / JME / CJUN / MCET / MCKE / McKE / MCKA / TAG-1 / Sec / FAST / cmi-1 / IL-1 bets / TN7 / FTK / Aps/ / p55 / ETS / C-Myc / IL-2 / IL-2 reseptor / NF-kappa B / TN7F-1 / TRAE / Apo-2L / BR4 / death receptor / DR3 / NR2 / DR3 / DR1 / bed / DR1 / Bd8-2 / TGF / griss / bid / FAN / perforin / Tas-L / Tag-1 / decay receptor / wd-1 / NGF receptor / growth factor / NAB

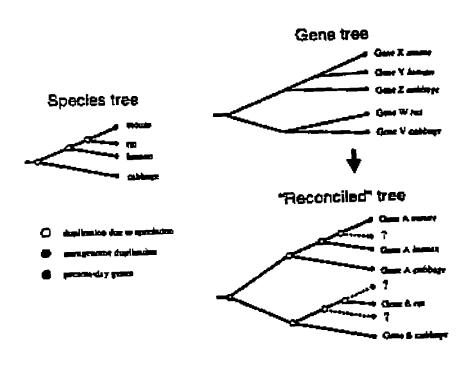


FIGURE 5

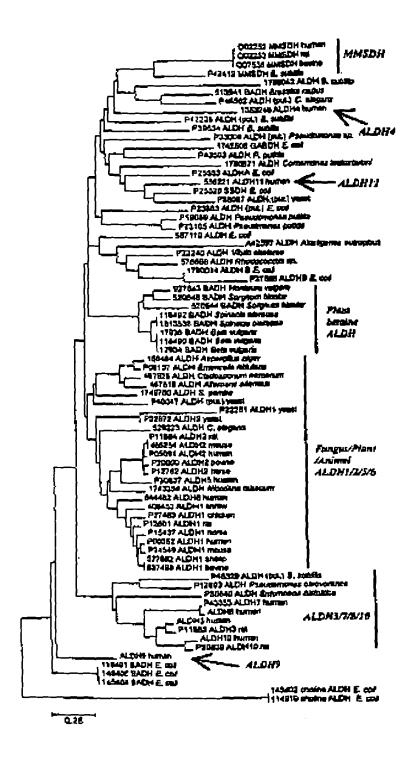


FIGURE 6

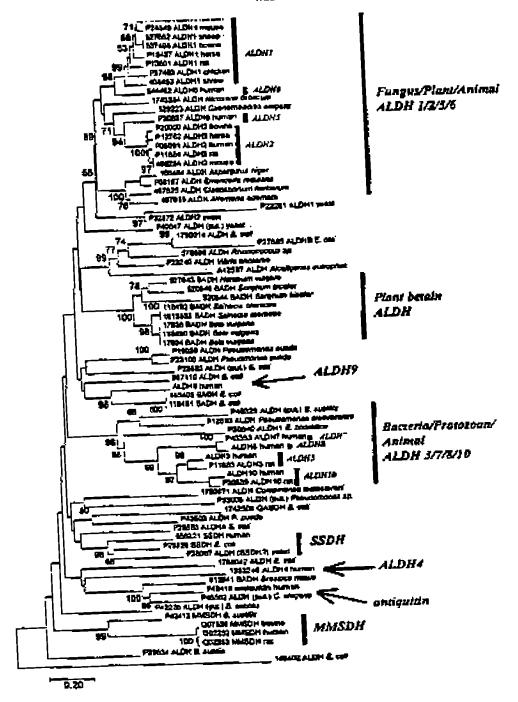


FIGURE ?

FIGURE 8

Start with Start with Start with a single Biological system a gene family a single gene Reconstruct a "network" of interacting genes and proteins Identify a set of key domains and motifs Search for related motifs in databases of known organisms Identify members of multigene families Compute phylogenetic trees Paralogous nitrorks Identify clusters of paralogous genes, identify paralogous and orthologics fienvorks Minimum meneral Parelogous networks in human يهاججه وبشيطانا

Compare regulatory schemes, identify genes that are known in one but missing in another system.

Find the genes using experimental (echniques.

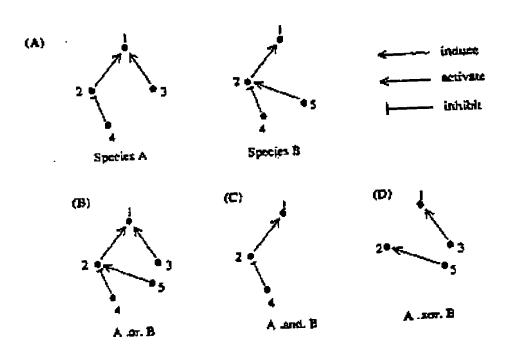


FIGURE 4

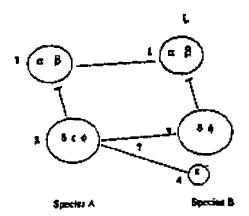


FIGURE 10

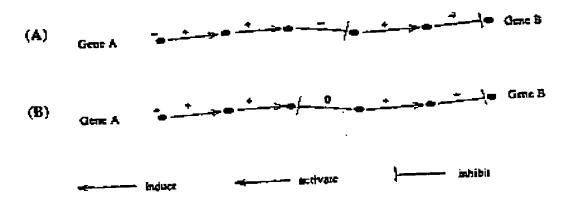


FIGURE II

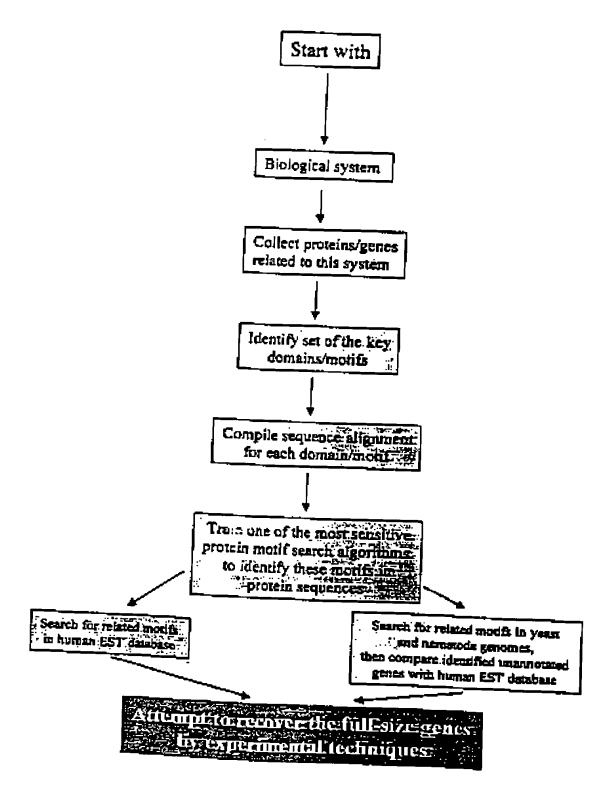


FIGURE 12.

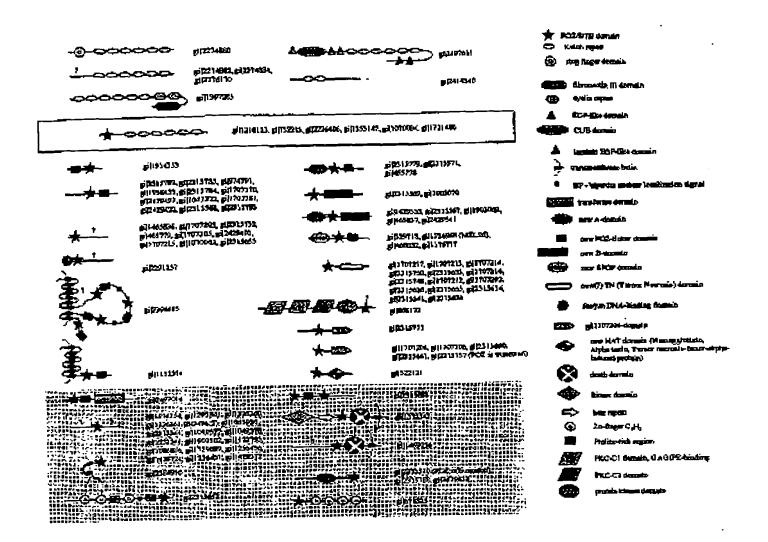


Figure 13

>qi122107661qb|AA4812141AA481214 ha34e02.c> NCI_CGAY_BCB\ Homo mapiena cBAA dlone JAAGE1813187 5' mimilar to WP:WD7A12.4 CE03795 1, nRNA amquence [Homo mapiena] CATGGCTTCCTGGACACCCAACCTGCCATCCGGGAGACCACTTTCCACGGCTACAGGCCAAAGATGAACAC AGCTGAACGAGCCCAACCTCAATGTGGAGCTGATGAACACTTTTCCACGGCTACAAGACCAAAGATGAACAC GOGCCCCATCGGCTACCTCAATGTGGAGCACTTGGGCAAAAATCGGCTACTACCTCAGTGCTAGCACCAGA CACAGGGTCCTTACCTCTGGCCTCAGGCCACAACCTCTACTCAATGAACGACTGTGCCCAGAAGATCCTGCCTTGCTC TGCTGGGCTTTGCTGCCCCCACAACCTTCTACTCAATGAACGACTGTGCCCAGAAGATCCTGCCTTGTGCT CTGCGGCTTCACTGTAGATCCTGAGAAAATCCGTGGGGACCAGAGGATCCTGCCCAGA

>gs||349211(gb|N51857|N51957 zc45f01.ri &osres_semescent_fibroblasts_NoHSF Homo sepiens <DNA clone image:325273 5', mRNA sequence (Homo sepiens) certosastrosgoccatrotosgoccatrotoccatrotoccatrotocatrotocatrotocatrotocatrotoccatro

Figure 14 A

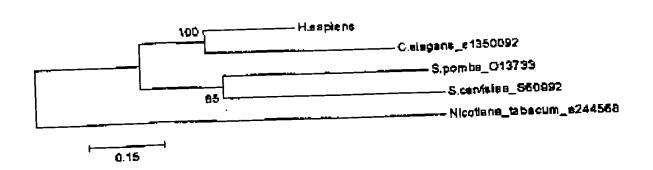


Figure 14B

EASE COUN'	r 405	a 545. c	493 g	278 t	6 others	
origin						
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61	ggayttctgt	cggcacaagg	tgctgcccca	gstgstgacc	geettegagt	teggenatge
121	tggggccgtt	gteeteaege	-ccctcttcaa	ggtgggcaag	ttcctqagcg	ctgaggagta
					tccactgacc	
241	catecgeste	ctgcagcaga	tggagcagtt	catocaptec	cttgacgage.	cascagtona
301	caeceagate	tteccecacg	togtacatgg	cttcctggac	accuacecto	.ccat ccggga
361	geagaeggte	Bagtccatgc	tgctcctggc	cccaaagetg	vacaeddcca	acctcaatot
					describable	
481	Carcaccaca	gtetacetag	gcmanategg	ctcctacctc	agigotagoa	ccagacacag
					tttgcaccet	
					atgaacgact	
					Beatcigtgo	
					gtqtcqqaqq	
					cetggcatgg	
					teacetees	
901	topcacecaa	ccactgcccc	aacagaaacc	aacattcccc	aaagacccac	gcctgaagga
					caacctcagg	
1021	acgetgggggg	aggacaagga	cacagcagag	gacagcagca	ctpctgscag	etgggacgac
1081	quagactqqq	desacetada	desdasdace	gagtotgtgt	tggcccagca	ggacgactog
						Capatectec
1201	adatecees	agtocgactg	gageagetgg	gearctgagg.	getectggga	acagggctgg
1261	caggagccaa	geteccagga	gecacetyst	.gacggtacec	ggetggeeag	cgagtateac
1321	tggggtggcc	Cagagt ccag	cqacaagggc	gaccccttcg	ctacectgtc	tgcacqtccc
1381	agcaccc#@C	cdadòccada	ctcttggggt	gaggacaact	gggagggcct	ogagactgac
						gcgggagatg
						gcccggaage
						cagatgtatt
						tecatearce
		azattctett				
H	-					

Figure 14C

D 10 15 20 25 30

1 SRSXOKFFQELSKSLDAFPEDFCRHKVLPQ

31 LLTAFEFGNAGAVVLTPLFKVGKFLSAEEY

61 QQKIIPVVVKMFSSTDRAMRIRLLQQMEQF

91 IQYLDEPTVNTQIFPHVVHGFLDTNPAIRE

121 QTVKSMLLLAPKLNEANLNVELMKHFARLQ

151 AKDEQGPIRCNTTVCLGKIGSYLSASTRHR

181 VLTSAFSRATRDPFAPSRVAGVLGFAATHN

211 LYSMNDCAQKILPVLCGLTVDPEKSVRDQA

241 EKAXRSFLSKLESVSEDPTQLEEVEKDVHA

Figure 14 D

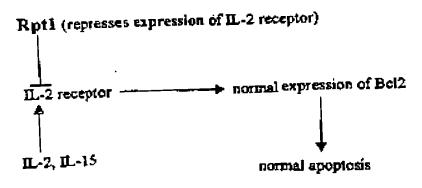
>sp[P15533]RPT1_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-1r [Mus musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15

Activated CD4+ T-cells



When rpt1 is knocked out:

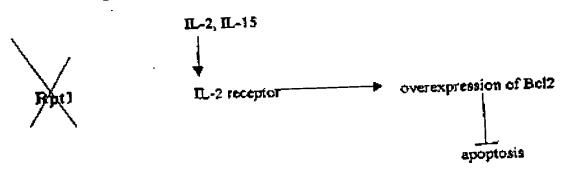


Figure 16

TALKSTH 2.0.8 [Jan-05-1989]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Behälfer, Jinghul Shang, Ehang, Webb Miller, and David J. Lippan (1997), "Gapped \$1.55 and \$61-81.85": a new gameration of protein database search programs", Nucleic Acida Res. 25:3889-3402. Querye q1/2137498|Med3m (205 letterm) gb;aA278224;AA278284 #877006.21 HCI_CGAP_GCG1 Homo sepiene eDHA clone 1MAGC:7D2520 5* ELOGIAT TO TREGILERIAT GILBRIET MEX-INTERACTING TRANSCRIPTIONAL ALERESSOR. , Congth # 430 Score - 205 bits (526), Expent = 1e-53 Identities = 104/124 (836), Positives - 118/124 (924), Gaps - 1/124 (08) Exame = +2 Outry: 1 Metyminicaligareflerrerprehemasicphhapotycrkkreelcapulinagra 60 MEPHASNIGVILLQAREFLERRERENGYASICOH SOG + RRHK P QARGA +8GRS SUJCt: 56 MEPHASNIGVILLQAREFLERRERENGYASICOHRSPOPIHERROREPGARGAGGGAS 235 Query: 61 VHNELEXARRAQLKROLEGIROGMPLGVDCTRYTTPLEIL-RARVHIONIEDGEGGARRIX 119 VHNELEKÄRRAGLKROLE+L+QQMPLG DC RYTYLSLL RARFHIGKLE+QEQ+AR+LK SOJCE: 236 VHNELEKRRRADLKRELERLKOOMPLOGOCAAYT7LELLKRARWHIOXILEOGGOAAAQLK 416 Query: 120 EKDES 124 C+F84 Spict: 416 ERLR7 #30 65] |CD2407(CD2407 HUMG50D12279, Human Game Signature, 3'-directed cDNA asquence. Length - 340 Score = 97.5 bits (239), Expent = 6e-20 Identities - 81/85 (808), Positives - 56/63 (878) query: 108 KOOSLOOGLEGLOGGLEGARERCALRADELDSBOLSFERSOSDOLDLEVDVENGVEGTETE 184 KOOSLOT OLTOL OA ERERLAADSLOSSELSSERSDSOOGTLEVIIVETLVIG S E BOJET: 45 KOOSICHOMOLRGLADAAERERIRADSLD&SGLSSERSDSDOFFLEVDVESLVFGGERE \$24

Figure 17A

Query: 185 LLQ 187 LL+ SMCT: 235 LLR 293

Base Coun' Drigin	r 130	в 234 с	258 g	106 t	5 others
1	cagoogottg	cteaggeagg	caccctagge	egeagteege	caggetyteg ceparatyga
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					tectcaggec tetectetga
541	gegetcagae	teagaccaag	aggagetgga	ggtggatgtg	gagagestgg tgtttggggg
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721	aageeeaett	tnc			

Figure 17B

C

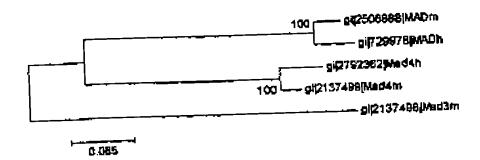
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D	
q1 7506H48 NAUS q1 77997 10000 q1 77997 2 MadEX q1 77997 2 MadEX q1 23 578 9 MadSa MadSh Potativa	-Marty Capper of Proposition of Statement of Chrocked Admicroples Rand Inches 1978 (1988) 1982 (1982) 1972 (1987) 1973 (1988)
91 (350688) (MACH 45 (729978) (MACH 91 (2792342) (MacHh 91 (3527498) (MacHh 41 (1547498) (MacHh 1467); Potation	######################################
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Figure 17 C-D

Α.



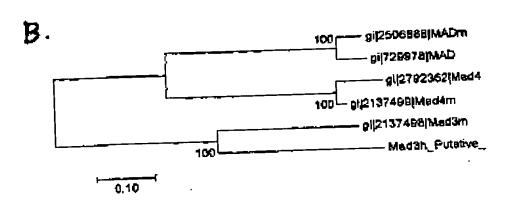


Figure 18-A-B

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% revised March 17, 2000
            LEXICON OF SUBSTANCES AND STRUCTURES
:-multifile(phrase/5).
:-multifile(wdef/3).
:-unknown( ,fail).
phrase('[',protein, ['[',gamma,']','-',aminobutyric, acid, a], 'GA
BAA', r}. % ?
phrase('[',smallmolecule, ['',zeta,')',1, subunit], '[zeta]1 subu
nit', r}. % ?
phrase(116, protein, [116,'-',kd,fyn,'-',associated,protein],'116-k
D Fyn-associated protein', r).
phrase(116, protein,[116,'-',kd,protein], 'l16-kd protein',r).
phrase(3,protein, [3,'-',kinase,'-',akt], '1-kinase-Akt',r).
phrase (ability, affirmation, [ability, to], (], r).
phrase (agc, protein, [agc, protein, kinases], 'AGC', r).
phrase(akt,protein, (akt, mutant), 'Akt mutant', r).
phrase (alternative, substance, [alternative, ntf], 'alternative NTF', r
phrase (antibody, protein, [antibody, to, phosphotyrosine], 'anti-phosp
hotyrosine',r).
phrase (antigen, complex, [antigen, receptor], 'antigen receptor', r).
phrase(ap, protein, [ap, '-', 1], 'AP-1', r).
phrase (aspargine, site, [aspargine, '-', 141], 'aspargine-141',r).
phrase(b, cell, (b,cell], 'B cell', r).
phrase(b, cell, (b,cells), 'B cell', τ).
phrase(b, species,[b,lymphoblastoid,cells], 'B lymphoblastoid cell
phrase(b,cell, {b,lymphoblastoid,cells), 'B lymphoblastoid cells',r
phrase(b7, protein, [b7,'-','l'], 'B7-l',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV',r).
phrase (casp, protein, [casp, '-', 3], 'caspase-3', r).
phrase(caspase, protein, [caspase, '-', 3, family, protease], 'caspase-3
 family protease',r).
phrase(caspase, protein, [caspase, '-', 3, precursor], 'caspase-3 precur
phrase(caspase, protein, [caspase, '-', 3], 'caspase-3',r').
phrase {caspase, protein, [caspase, -, 3], 'caspase-3', r).
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Appendix A

Page 1

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phrase (caspase, protein, [caspase, '-', 6], 'caspase-6', r).
phrase (caspase, protein, [caspase, '-', 7], 'caspase-7', r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
r).
phrase(cleavage, site, [cleavage, site), 'cleavage site',r).
phrase(cleavage, substance, [cleavage, products], 'cleavage products',
r).
phrase(cooh, substance, [cooh, '-', terminal, fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crk1, complex.[crk1,'-',c3g,complex],'crk1-c3g complex',r).
phrase(dcp,protein,[dcp,-,1],'DCP-1',r).
phrase(did, negation, [did, not], not, r).
phrase(ebv, species, 'Epstein-Barr virus', r).
phrase (epstein, species, [epstein, '-', barr, virus], 'Epstein-Barr vi
rue',r).
phrase (familial, disease, [familial, alzheimer, '''', s, disease), 'famil
ial Alzheimer'''s disease',r).
phrase (gene, gene, [gene, encoding, interleukin, '~',2], 'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r'),
phrase(gtp, complex, [gtp, exchange, of, rapl], 'GTP exchange of Rapl',
r).
phrase (quanidine, protein, [quanidine, nucleotide, '-', releasing, fac
tor, c3g], 'guanidine nucleotide-releasing factor C3G1,r).
phrase (quanidine, small molecule, [quanidine, nucleotide], 'quanidine
 nucleotide',r).
phrase (guanosine, smallmolecule, [guanosine, triphosphate], 'guanosin
e triphosphate',r).
phrase (guanosine, smallmolecule, (guanosine, diphosphate), 'guanosine
diphosphate',r).
phrase(h4.cell,[h4.cell,line], 'H4 cell line',r).
phrase(h4,cell,[h4,human,neuroglioma,cells], 'H4,human,neuroglioma
,cells',r).
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb],'HA-[Delta]PHPK
B',r),
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,'}'],
                                                                'I[ka
ppa|B-[beta]',r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'),
                                                               'I (kap
pa]8-[alpha]',r).
phrase(i,protein, [i, '[',kappa, ']',b], 'I(kappa)B',r).
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Page 2

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phrase(ice,protein,[ice,'/',ced,'-',3),'1CE/Ced-3',r).
phrase(il, gene, [il,'-',2,gene), 'gene encoding interleukin-2', r
).
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in, state, (in, the, amergic, state), inactive, r).
phrase {inducible, cell, [inducible, h4, cell], 'inducible H4 cell', r
phrase {interleukin, protein, [interleukin, '-', 2], r).
phrase {interleukin, protein, (interleukin, '-', 3], 'interleukin-3
phrase (interleukin, protein, [interleukin, '-',1,beta,converting,enzy
me], 'interleukin-1 beta converting enzyma',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, [jurkat, cells], 'Jurkat cell', r). .
phrase(kif3a, protein, [kif3a, '/', 3, b], 'KIF3A/3B', r).
phrase(lbl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cells',r).
phrase(lbl,cell,[lbl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let,'-',23], 'Let-23', r).
phrase(may, probability, [may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3B',r).
phrase(myc, protein, {myc, '-', pdkl], 'Myc-PDK1',r}.
phrase (myc, protein, [myc, '-', p?0s6k], 'Myc-p?0s6k', r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r}
phrase(myr, protein, [myr, '-', akt], 'Myr-Akt', r).
phrase(n.protein, [n,'-'.methyl,'-',d,'-',aspartate, receptor], 'N
MDAR', r).
phrase(n.protein, {n,'-',methyl,'-',d,'-',aspartate], 'NMDA'},
phrase(native, cell, [native, h4, cell], 'native H4 cell', r).
phrase(nf, protein, [nf,'-','[',kappa,']',b],
                                                'NF-[kappa] &', r),
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2.substance.[nh2.'-'.terminal.fragment], 'NH2-terminal fr
agment', r).
phrase(nih, cell, [nih,'-',3,t3,fibroblasts], 'NIH-3T3 fibroblasts'
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
phrase(normal, substance, [normal, ntf], 'normal NTF', r).
phrase(nuclear, protein, [nuclear, factor, kappa, b],'NF-[kappa]B'
phrase(pl50Glued,protein,[pl50Glued,-,arpl],'pl50Glued-Arpl',r).
phrase(phosphate, phosphorylate2, [phosphate, incorporated, into],
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phosphorylate, r). phrase (phosphatidylinositol, smallmolecule, [phosphatidylinositol, 1 ,',',4,',',5,'-',triphosphate), 'phosphatidylinositol 1,4,5-tripho aphate',r). phrase (phosphoinositide, protein, [phosphoinositide, '-', dependent, $^{\mathsf{PDKl}}$ ', $^{\mathsf{r}}$). protein, kinase), phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip ase C-1', r): phrase(poly,protein,[poly,'{',adp,'-',ribose,')',polymerase],'poly (ADP-ribose) polymerase',r}. phrase (polyvinylidene, structure; [polyvinylidene, difluoride, memb ranes), 'polyvinylidene difluoride membranes', r), phrase(presentlin, protein,[presentlin,1],'presentlin l',r). phrase(presentlin, protein, [presentlin, 2], 'presentlin, 2', r). phrase(productively, state, [productively, stimulated], active, r). phrase(protein, protein, [protein, tyrosine, kinase], 'protein tyrosi πe kinase', r). phrase(protein, protein, [protein, kinase, c], 'protein kinase C', r). phrase(ps2, substance, [ps2, '-', ctf], 'presentlin 2 COOH-terminal fra phrase(ps2.substance,[ps2,cleavage,fragment], 'presenilin 2 cleava ge fragment', r). phrase(pvdf, structure, [pvdf, membranes], polyvinylidene difluori de membranes',r). phrase(raf, protein, [raf,'-',1], 'Raf-1', r). phrase(raf, protein, [raf, '-',1], 'Raf-1',r). phrase(rap1.complex,[rap1,'-',gtp), 'Rap1-GTP',r). phrase(requirement, need2, [requirement, for], need,r). phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r). phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r). phrase(serine, substance, [serine, residues], 'serine residues', r phrase(src, domain, [src, homology, 2], 'Src homology 2',r). phrase(src, domain, (src, homology, 3], 'Src homology 3',r). phrase(srebp,protein,(srebp,'-',1), 'sterol-regulatory element bin ding protein 1',r). phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin ding protein 2',r). phrase(sterol, protein, (sterol, '-', regulatory, element, binding, prote in,1], 'sterol-regulatory element binding protein 1',r).

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phrase(sterol, protein, [sterol, '-', regulatory, element, binding, prote

in,2], 'sterol-regulatory element binding protein 2',r).

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phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7-1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex,(t,'~',cell,receptor),'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'.',cell,antigen,receptor),'T-cell antigen red
eptor', r}.
phrase(threonine, aminoacid, [threonine, 229], 'threonine 229', r)
phrase(transcription, protein, [transcription, factor], 'transcript
ion factor', r}.
phrase(trypan, smallmolecule, 'trypan blue', r).
phrase(wt, protein, [wt, skt], 'WT Akt', r).
phrase(zap, protein, [zap, '-', 70], 'ZAP-70', r).
phrase(zdevd, smallmolecule, [zdevd, '-', fmk], 'zDEVD-fmk',r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin,protein,actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad, disease, 'Alzheimer'''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef(amergic, state, inactive).
wdef(amergic,etate,inactive).
wdef(anergy, state, inactive).
wdef(antibody,complex,antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef(apoptosis,process,apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase, protein, caspase).
wdef(caspase, protein, caspase).
wdef(cbl, protein, 'Cb1').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol, smallmolecule, cholesterol).
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wdef(cpp32,protein,'CPP32').
 wdef(crkl, protein, 'CrkL').
 wdef(ctf, substance, 'COOH-terminal fragment').
 wdef(cytokine, smallmolecule, cytokine).
 wdef(cytosol, structure, cytosol).
 wdef(djnk,protein, 'DJNK').
 wdef{djun, protein, 'DJun'}.
 wdef (dynamitin, protein, dynamitin).
 wdef{erk, protein, 'ERK'}.
 wdef(eto,smallmolecule,'ETO').
 wdef (etoposide, small molecule, etoposide).
 wdef(fad, disease, 'familial Alzheimer'''s disease').
 wdef(fyn, protein, 'Fyn').
 wdef(gdp, smallmolecule,'GDP').
 wdef (gelaolin, protein, gelsolin).
 wdef(gp120, protein, 'gp120').
 wdef (grb2, protein, 'Grb2').
 wdef(gst, protein, 'glutathione S-transferase').
 wdef(qtp, smallmolecule, 'GTP').
 wdef(hsp70,protein,'HSP70').
 wdef(human, species, human).
 wdef(ikk, protein, 'IKK').
 wdef(inactivated, state, inactive).
 wdef (inactive, state, inactive).
 wdef(jnk, protein, 'JNK').
 wdef(jnk, protein, 'JNK').
 wdef(jnk2, protein, 'JNK2').
 wdef(kap3,protein,kap3).
 wdef(kdakt, protein, 'KDAkt').
 wdef(kinase, protein, kinase).
 wdef(kinectin, protein, kinectin).
 wdef(klc,protein,klc).
, wdef(lamin,protein,lamin).
 wdef (myosins, protein, myosins).
 wdef(nmdar.protein, 'NMDAR').
 wdef(nmdar2b, protein, 'NMDAR2B').
 wdef(ntf, substance, 'NH2-terminal fragment').
 wdef(p70s6k, protein, p70s6k).
 wdef(p78s6k, protein, p78s6k).
 wdef(parp,protein, 'poly(ADP-ribose)polymerase').
 wdef(pdk1, protein, 'PDK1').
 wdef (peptides, protein, peptide).
 wdef(pkb, protein, 'PKB').
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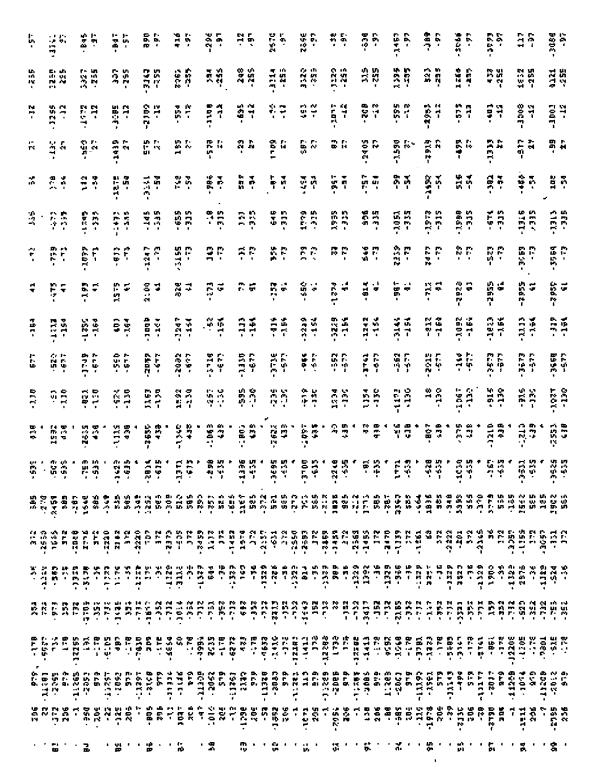
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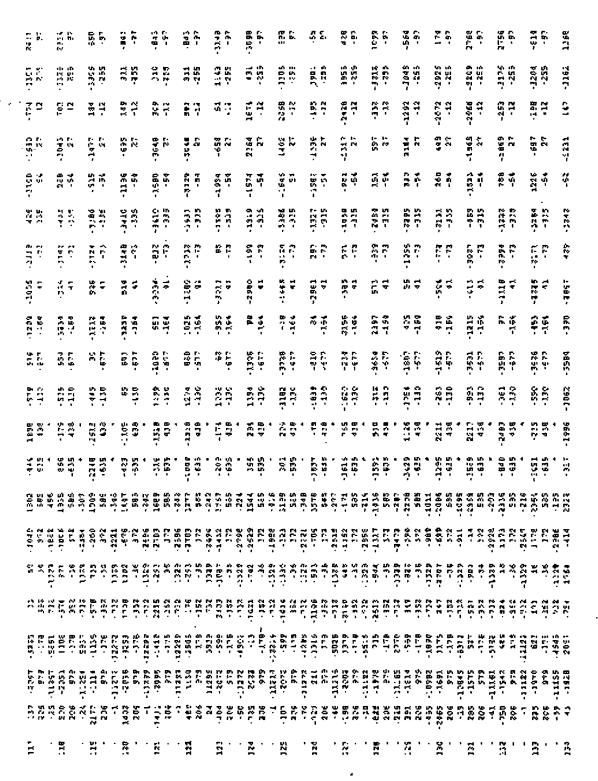
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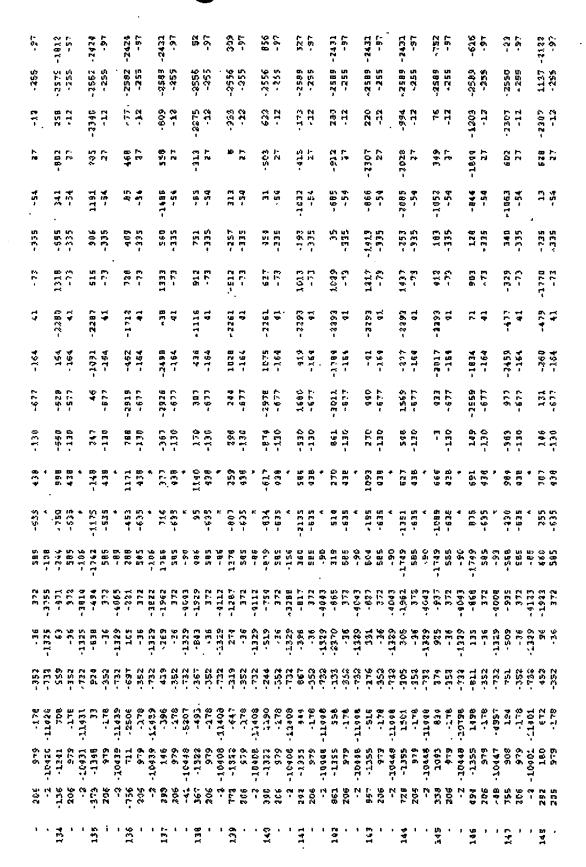
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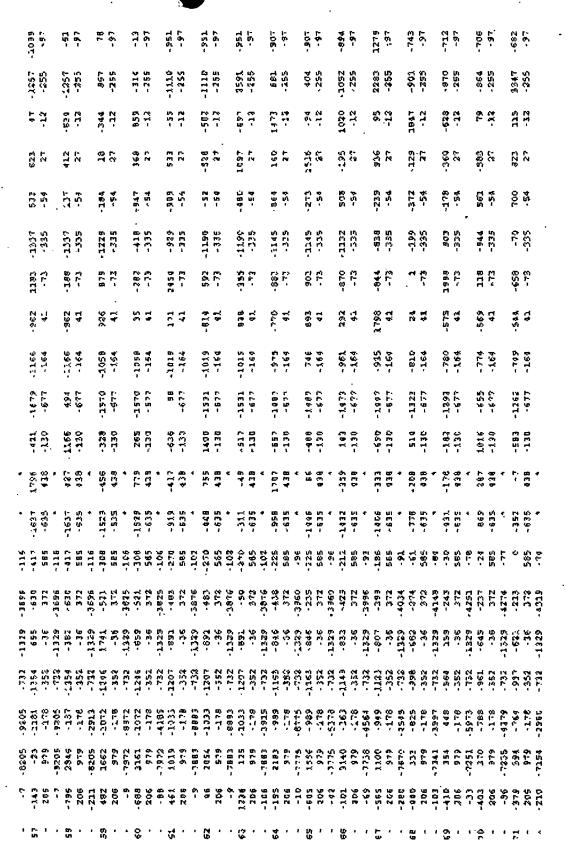
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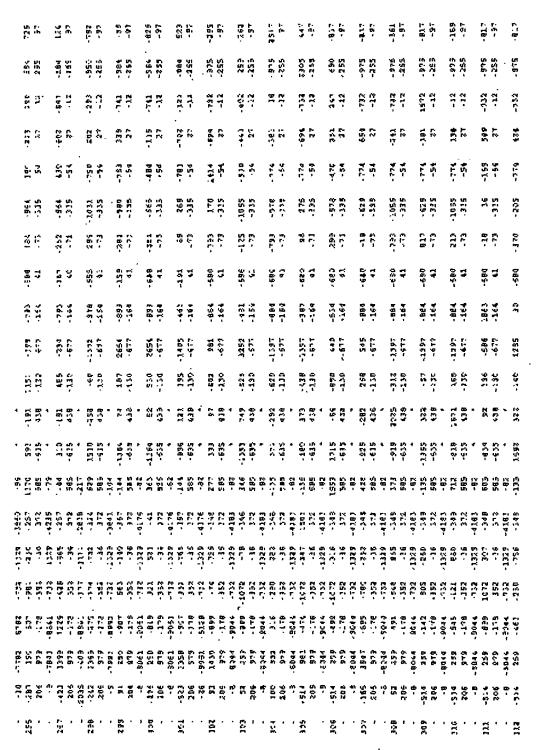
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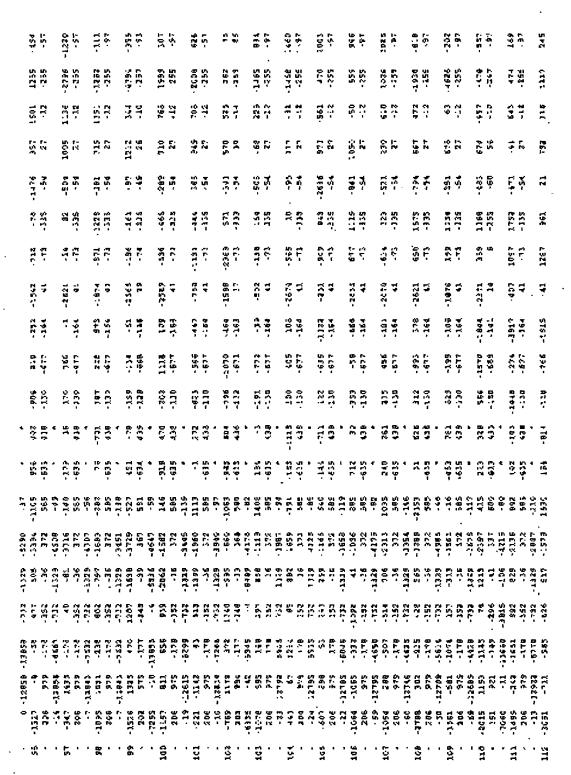
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wdef {psl, protein, 'presenilin 1').
wdef(ps2, protein, 'presenilin 2').
wdef(rapl, protein, 'Rapl').
wdef(ras, protein, 'Ras').
wdef(receptors, substance, receptor).
wdef(rela, protein, 'RelA').
wdef (residues, substance, residue).
wdef(responsive, state, active).
wdef($6, protein, 'S6').
wdef(selectively, constraint, selective).
wdef(ser112, site, 'Ser112').
wdef(ser136, site, 'Ser136').
wdef(ser32, smallmolecule, 'Ser32').
phrase(ps1, protein
wdef(ser36, smallmolecule, 'Ser36').
phrase(ps1, protein, [ps1,'-',ctf], 'ps1-ctf',r).
wdef(sh2,domain, 'SH2').
wdef(sh3,domain,'$H3').
wdef(shc, protein, 'Shc').
wdef{signalsome, complex, signalsome).
wdef (sites, site, site).
wdef(sos, protein, 'Sos').
wdef(staurosporine, smallmolecule, staurosporine).
wdef(sts, smallmolecule, 'STS').
wdef(tcr, complex, 'T-cell receptor').
wdef (tetracycline, smallmolecule, tetracycline).
wdef(thr229, aminoacid, 'Thr229').
wdef (thr308, aminoacid, 'Thr306').
wdef(thr389, aminoacid, 'Thr389').
wdef (threonine, aminoacid, threonine).
wdef(tyrosine, aminoacid, tyrosine).
wdef {unresponsive, state, inactive}.
wdef (unstimulated, state, inactive).
wdef(zvad, smallmolecule, 'zVAD').
```

```
% lexsyn.pat
% revised March 17, 2000
                 SYMTACTIC LEXICON FOR ACTIONS
a Contains syntactic entries for action type words and phrases
% symp (+Word1.+Wordlist,+Syn)
% symp: Wordl is first word of phrase, Wordlist is list of words i
n phrase
& symp: Sym is symtactic categorey
% synw(+Word.+Syn) is same as synp except there is no wordlist
symp (account, [account, for], v).
synp (account, [account, for], vp).
symp (accounted, [accounted, for], ved).
symp(accounted, [accounted, for], ven).
symp(accounting, {accounting, for), ving).
symp (accounting, (accounting, for), n).
eynp (accounts, [accounts, for), vp).
eynp(add, [add, up], vp).
symp (add, [add, up],v).
symp (added, [added, up],, ved).
symp (added, (added, up), ven).
eynp (adding, [adding, up], n).
symp(adding, [adding, up], ving).
symp (adds, [adds, up], vp).
symp(am, [am,a,means,of, producing],vp).
symp(am, [am, due, to], vp).
symp(are, {are,a,means,of, producing), vp).
symp(are, (are, due, to), vp).
symp(as, [as, a, result, of], prep).
symp(attributable,[attributable,to],vp). % ?
symp(attributed, [attributed, to], ven).
symp (based, [based, on], ven).
synp (based, [based, upon], ven).
symp(be, [be,a,means,of, producing),v).
symp (be, [be, due, to], v).
symp(because, [because, of], prep).
synp(been, [been, a, means, of, producing), ven).
symp (been, [been, due, to], ven).
synp(being, [being,a,means,of, producing],n).
symp(being, [being, a, means, of, producing], ving).
```

Appendix B

```
symp(being, [being,due,to],n).
symp(being, [being, due, to], ving).
symp(caused, (caused, by), ved).
symp(caused, [caused,by],ven).
symp(convey, [convey, a, signal], v).
symp(convey, (convey, a, signal), vp);
symp (conveyed, [conveyed, a, signal], ved).
symp(conveyed, [conveyed, a, signal], ven).
symp(conveying, (conveying, a, signal), ving).
symp(conveying, [conveying, a, signal], n).
symp(conveys, [conveys,a, signal], vp).
symp(dissociate, [dissociate, from], vp).
synp(dissociate, [dissociate, from], v).
symp(dissociated, [dissociated, from], ved),
symp{dissociated, [dissociated, from], ven].
symp (dissociates, [dissociates, from], vp).
symp(dissociating, [dissociating, from], n).
symp{dissociating, [dissociating, from], ving}.
symp (dissociation, [dissociation, from], n).
symp(down,[down,'-',regulate],v).
synp(down, [down, '-', regulate], vp).
                                     % A down-regulates B
                                                                      A
 --> B
symp{down, [down, '-', regulated], ved).
symp(down, [down, '-', regulated], ven).
symp(down, [down, '-', regulates], vp).
symp(down, [down, '-', regulating], n).
symp(down, [down, '-', regulating], ving).
symp(down,[down,'-',regulation],n).
symp(due, [due, to, the, fact, that], adj).
synp{due,[due,to],adj). % ?
symp(form, [form, complex], v).
symp(form, [form, complex], vp).
symp(formation,[formation, of, complex],n).
symp{formed, [formed, complex], ved).
symp(formed, [formed, complex), ven).
symp{forming, [forming, complex],n).
symp(forming, [forming, complex], ving).
symp(forms, {forms, complex}, vp).
symp(had, [had,an,active,role,in],ved).
symp(had, [had,an,active,role,in],ven).
symp(has, [has,an,active,role,in],vp).
symp(have, [have, an, active, role, in], v).
symp(have, [have,an,active,role,in],vp).
```

```
symp(having, (having, an, active, role, in), n).
symp(having, [having, an, active, role, in], ving).
symp(is, [is,a,means.of, producing].vp).
symp(is, [is,due,to],vp).
symp (functions, [functions, as, a, negative, regulator, of], vp).
symp (function, [function, as, a, negative, regulator, of], vp).
symp(lead, [lead,to],v).
symp(leads, [leads,to],vp).
symp(leading, [leading,to],n).
symp(leading, [leading,to], ving ).
eynp(leads, [leads,to].vp ).
symp(led, [led, to], ved).
symp(led, [led, to], ven).
eymp(may, [may, be, responsible, for], vp).
symp(mediate,[mediate, a, signal], v).
                                              %A mediates a signal to
synp(mediate, [mediate, a, signal], vp).
synp (mediated, [mediated, a, signal], ved).
synp(mediated,[mediated, a, signal], ven).
symp(mediates, [mediates, a, signal], vp).
symp (mediating, [mediating, a, signal], n).
symp(mediating, [mediating, a, signal], ving).
symp(mediation, [mediation, of, a, signal], n).
symp(n, (n, '-', acetylate), v).
symp(n, [n, '-', acetylate), vp).
symp(n, [n, '-', acetylated], ved).
symp(n, [n, '-', acetylated], ven).
Bynp(n, (n, '-', acetylates).vp).
symp(n, [n, '-', acetylating), n).
symp(n,[n,'-',acetylating],ving).
symp(n, [n, '-', acetylation], n).
symp(n, [n, '-', acylate], v).
symp(n, [n, '-', acylate], vp).
symp (n, (n, '-', acylated), ved).
symp(n, [n, '-', acylated], ven).
symp (n, [n, '-', acylates], vp).
symp(n, [n, '-', acylating], n).
symp(n, [n, '-', acylating], ving).
symp(n, \{n, '-', acylation\}, n).
symp(n, [n, '-', glycosylate), v).
synp(n, [n, '-', glycosylate], vp).
symp(n, [n, '-', glycosylated), ved).
symp(n, [n, '-', glycosylated], ven).
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symp(n, [n, '-', glycosylates], vp).
symp {n, [n, '-', glycosylating], n}.
symp {n, [n, '-', glycosylating], ving).
symp(n, [n, '-', glycosylation], n).
symp (n, (n, '-', terminal, proteolysis), n).
symp(o, [o, '-', glycosylate], v).
symp(o, (o, '-',glycosylate),vp).
symp(o, (o, '-', glycosylated), ved).
symp(o, [o, '-', glycosylated], ven).
symp(o, [o, '-', glycosylates], vp).
symp(o, (o, '-'.glycosylating),n).
symp(o,[o,'-'.glycosylating],ving).
symp(o, [o, '-', glycosylation), n).
symp(only, (only, after), prep).
symp(prolyl, 'prolyl,'-',4,'-',hydroxylate],v ).
symp(prolyl, (prolyl, '-',4,'-',hydroxylate),vp).
symp(prolyl, [prolyl,'-',4,'-',hydroxylated],ved ).
symp(prolyl, [prolyl,'-',4,'-',hydroxylated],ven ).
synm(prolyl, [prolyl, '-',4,'-',hydroxylates],vp).
symp{prolyl, (prolyl,'-',4,'-',hydroxylating],n }.
symp(prolyl, [prolyl,'-',4,'-',hydroxylating],ving ).
symp(prolyl, [prolyl,'-',4,'-',hydroxylation],n).
symp(result, [result, from], v).
symp(result, (result,from),vp).
symp(result, [result, in], v).
symp(result, [result, in], vp).
symp (resulted, [resulted, from], ved).
symp {resulted, [resulted, from], ven}.
symp(resulted, [resulted,in],ved).
symp(resulted, [resulted, in], ven).
symp(resulting, [resulting,from],n).
symp (resulting, [resulting, from], ving).
symp(resulting, [resulting, in], n).
symp {resulting, [resulting, in], ving).
symp(results, [results, from], vp).
symp(results,[results,in],vp).
symp(set, [set, free],v).
symp(set, [set, free], v).
symp(set, [set, free], ved).
symp(set, [set, free], ved).
symp(set, [set, free], ven).
synp(set, [set, free].ven).
aynp(set, [set, free], vp).
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eynp(set, [set, free], vp).
symp(sets, [sets, free], vp).
synp(sets, [sets, free], vp).
eynp(setting, [setting, free], n).
symp(setting, (setting, free),n).
symp(setting, [setting, free], ving).
symp(setting, [setting, free), ving).
symp(suppress, [suppress, activity, of],v).
symp(suppress, [suppress, activity, of], vp).
symp(suppressed, [suppressed, activity, of), ved).
symp(suppressed, [suppressed, activity, of], ven).
symp(suppresses, [suppresses, activity, of], vp).
symp (suppressing, [suppressing, activity, of], n).
symp(suppressing, [suppressing, activity, of], ving).
symp(suppression, [suppression, of, activity, of), n).
symp(switch, [switch, on, the, activity, of], vp).
symp(switched, (switched, on, the, activity, of), ved).
symp(switched, (switched, on, the, activity, of), ved).
symp(switched,[switched, on, the, activity, of], ved).
symp(switched,[switched, on, the, activity, of], ved).
eymp(switched, [switched, on, the, activity, of), ved).
symp(switches, (switches, on, the, activity, of), vp).
symp(up, [up, '-', regulate], v). % A up-regulates B B --> A
eymp(up, |up, '-', regulate), vp). % A up-regulates B B --> A
symp (up, (up, '-', regulated), ved).
synp (up, (up, '-', regulated), ven). % A up-regulates B B --> A
symp(up, [up, '-', regulates], vp).
symp (up, {up, '-', regulating), ving). % A up-regulates B B --> A
symp(up, [up, '-', regulation], n).
symp(was, [was,a,means,of, producing], ved).
symp(was, [was,due,to], ved).
eymp(were, [were,a,means,of, producing], ved). % ?
symp(were, [were, due, to], ved).
synw(acetylate, v).
symw(acetylate, vp).
synw(acetylated, ved).
synw(acetylated, ven).
synw(acetylates, vp).
synw(acetylating,n).
synw(acetylating, ving).
synw(acetylation,n).
synw(activate, v).
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synw(activate, vp).
symw(activated, ved).
synw(activated, ven).
synw(activates, vp).
synw(activating,n).
synw(activating, ving).
synw (activation, n),
synw(add,v).
synw(add, vp).
synw(added, ved).
aynw(added,ven).
synw(adding,n).
synw(adding, ving).
synw(addition,n).
synw(adds, vp).
synw(after,prep).
synw(aggregate , v).
synw(aggregate ,vp).
synw(aggregated , ved).
synw(aggregated , ven).
synw(aggregates, vp).
synw(aggregating ,n).
synw(aggregating ,ving).
synw(aggregation ,n).
synw(arrest,n).
symw(arrest,v).
synw(arrest, vp).
synw(arrested, ved).
synw(arrested, ven).
synw(arresting,n).
synw(arresting, ving).
synw(arrescs, vp).
synw(associate, v).
synw(associate, vp).
synw(associated, ved).
synw(associated, ven).
Bynw(associates, vp).
synw (associating, n).
synw(associating, ving).
synw(association, n).
synw(attach , v).
synw(attach, vp).
synw(attached , ved).
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synw(attached , ven) .
gynw(attaches, vp).
synw(attaching ,n).
synw(attaching , ving).
synw(attachment,n).
eynw(bind,v).
synw(bind, vp).
synw(binding,h).
synw(binding, ving).
synw(binds, vp).
synw(block, v) .
synw(block, vp).
synw(blockage,n).
synw(blocked, ved).
synw(blocked, ven).
synw(blocking,n).
synw(blocking, ving).
synw(blocks, vp).
synw(bound, ved).
synw(bound, ven).
synw(break, v).
synw(break, vp).
synw(breakage, n).
synw(breaking,n).
synw(breaking, ving).
synw(breaks, vp).
synw(broke, ved).
synw(broken, ven).
eynw(catalyzation, n).
synw(catalyze, v).
aynw(catalyze, vp).
synw(catalyzed, ved).
synw(catalyzed, ven).
synw(catalyzes, vp).
synw(catalyzing, n).
synw(catalyzing, ving).
synw(causation,n).
synw(cause,n).
synw(cause, v).
synw(cause, ven).
synw(cause, vp).
synw(caused, ved).
synw(causes, vp).
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eynw(causing, n). .
avnw(causing, ving).
synw(cleavage,n).
synw(cleave, v).
synw(cleave, Vp).
synw(cleaved, ved).
synw(cleaved, ven).
synw(cleaves, vp).
symw(cleaving, n).
synw(cleaving, ving).
eynw(coimmunoprecipitate ,v).
synw(coimmunoprecipitate, vp).
synw(coimmunoprecipitated , ved).
synw(coimmunoprecipitated , ven).
synw(coimmunoprecipitates, vp).
synw(coimmunoprecipitating ,n).
synw(coimmunoprecipitating , ving).
synw(coimmunoprecipitation ,n),
synw(combination ,n).
synw(combine , v).
synw(combine , vp).
synw(combined , ved).
synw(combined , ven).
synw(combines, vp).
synw(combining ,n).
synw(combining , ving).
synw(conjugate ,v).
synw(conjugate , vp).
synw(conjugated , ve).
synw(conjugated , ved).
synw(conjugates, vp).
synw(conjugating ,n).
synw(conjugating , ving).
eynw(conjugation ,n).
synw(connect , vp).
synw(connect, v).
synw(connected , ve) . - -
synw(connected , ved).
synw(connecting , n).
synw(connecting , ving).
synw(connection ,n).
synw(connects, vp).
synw(constrain, v).
```

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gynw(constrain, vp).
eynw (constrained, ved).
synw (constrained, ven).
synw(constraining, n).
synw(constraining, ving).
synw(constrains, vp).
synw(constraint, n).
synw(coprecipitate,v).
synw(coprecipitate, vp).
synw(coprecipitated, ved).
synw(coprecipitated, ven).
synw(coprecipitates, vp).
synw(coprecipitating,n).
synw(coprecipitating, ving).
synw(coprecipitation ,n).
synw(copurification ,n).
synw{copurified , ved).
synw(copurified , ven).
synw (copurifies, vp).
synw(copurify , vp) .
synw(copurify, v).
synw(copurifying ,n).
synw(copurifying , ving).
synw(couple ,Vp).
synw(couple, v).
synw(coupled, ved).
synw(coupled, ven).
synw(couples, vp).
synw(coupling, n).
synw(coupling.ving).
synw(cut,n).
synw(cut,v).
synw(cut, ved).
synw(cut, ven).
synw(cut, vp).
synw(cuts, vp).
synw(cutting,n).
synw(cutting, ving).
synw(deactivate,v).
synw(deactivate, vp).
synw(deactivated, ved).
synw (deactivated, ven).
synw(deactivates.vp).
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synw(deactivating,n).
synw(deactivating, ving).
synw(deactivation,n).
synw(death,n).
synw (demethylate, v).
synw (demethy late, vp).
synw (demethy lated, ved).
synw (demethylated, ven).
synw(demethylates, vp).
synw(demethylating,n).
synw(demethylating, ving).
synw(demethylation, n).
synw(dephosphorylate, v).
synw (dephosphorylate, vp).
synw(dephosphorylated, ved).
synw(dephosphorylated, ven).
synw(dephosphorylates, vp).
synw(dephosphorylating, n).
synw(dephosphorylating, ving).
synw(dephosphorylation, n).
synw (die, v).
synw (die, vp).
synw (died, ved).
synw(died, ven).
synw(dies, vp).
synw(disassemble, v).
synw(disassemble, vp).
synw(disassembled, ved).
synw(disassembled, ven).
synw(disassembles, vp).
synw(disassembling, n).
synw(disassembling, ving).
synw (disassembly, n).
Bynw(discharge, n) .
synw(discharge, v).
synw(discharge, vp).
synw(discharged, ved):
synw(discharged, ven).
synw(discharges, vp).
eynw (discharging, n).
synw (discharging, ving).
synw(disengage, v).
synw(disengage, vp).
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synw (disengaged, ved).
synw{disengaged, ven}.
synw (disengagement, n) .
synw(disengages, vp).
synw (disengaging, n).
synw(disengaging, ving).
synw(divide, V).
synw (divide, vp).
synw (divided, ved).
synw{divided, ven}.
synw (divides, vp).
synw(dividing, n).
synw(dividing, ving).
symw (division, n).
synw(dying,n).
synw(dying, ving).
synw(enhance,v).
synw(enhance, vp).
synw (enhanced, ved).
synw(enhanced, ven).
aynw(enhancement, n) .
aynw(enhances, vp).
synw(enhancing,n).
synw(enhancing, ving).
synw(express,V).
synw(express, vp).
synw(expressed, ved).
synw(expressed, ved).
synw(expressed, ven).
aynw(expresses.vp).
synw(expressing.n).
synw(expressing,n).
synw(expressing, ving).
synw(expression, n).
synw(generate, v).
synw(generate, vp).
synw(generated, ved).
aynw(generated, ven).
aynw (generates, vp).
synw(generating,n).
synw (generating, ving).
synw(generation,n).
synw (hew, v).
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synw(hew,vp).
synw(hewed, ved)
synw (hewed, ven).
eynw(hewing,n).
synw(hewing, ving).
aynw(hews, vp).
aynw(hinder, v).
aynw(hinder, vp).
synw(hindered, ved).
aynw(hindered, ven).
. (n, garingen) aynw (hindering
synw(hindering, ving)...
synw(hinders, vp).
synw(hindrance,n).
synw(inactivate,v).
synw(inactivate, vp).
synw(inactivated, ved).
synw(inactivated, ven).
synw(inactivates, vp).
synw(inactivating,n).
synw(inactivating, ving).
synw(inactivation, n).
synw(incite, v).
synw(incite, vp).
synw(incited, ved).
synw(incited, ven).
synw(incitement,n).
synw(incites, vp)
synw(inciting, n).
synw(inciting, ving).
synw(induce,v).
synw(induce, vp).
synw(induced, ved).
synw(induced, ven).
synw(induces, vp).
synw(inducing,n).
synw(inducing, ving).
synw(induction, n).
synw (influence, n).
synw(influence, v).
synw(influence, vp).
synw{influenced, ved}.
aynw(influenced, ven).
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synw(influences,vp)...
synw(influencing,n).
synw(influencing, ving). % ?
synw(inhibit, v).
synw(inhibit.vp).
gynw(inhibited, ved).
aynw(inhibited, ven).
aynw(inhibiting,n).
synw(inhibiting, ving).
eynw (inhibition, n).
gynw(inhibits,vp).
synw (initiate, v).
synw(initiate, vp).
synw(initiated, ved).
synw(initiated, ven).
synw(initiates, vp).
synw(initiating,n).
eynw(initiating, ving).
synw(initiation, vp).
synw(instigate,v).
synw(instigate, vp).
synw(instigated, ved).
synw(instigated, ven).
synw(instigates, vp).
synw(instigating,n).
eynw (instigating, ving).
synw(instigation,n).
synw(interact,v).
synw(interact.vp).
synw(interacted, ved).
synw(interacted, ven).
synw (interacting, n).
synw(interacting, ving).
synw(interaction,n).
synw(interactions,n).
eynw(interacte,vp).
eynw(join , vp) .
symw(join,v).
synw(joined, ved).
symw(joined, ven).
. (a, paining, n) .
eynw(joining, ving).
eynw (joine, vp) .
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```
synw(juncture, n).
synw(liberate, v).
synw(liberate, vp).
eynw(liberated, ved).
synw(liberated, ven).
synw(liberates.vp).
 synw(liberating, n).
 synw(liberating, ving).
synw(liberation, n).
synw(limit,v).
synw(limit, vp).
synw(limitation, n).
synw(limited, ved).
synw(limited, ven).
synw(limiting,n).
synw(limiting, ving).
synw(limits, vp).
synw(link,n).
aynw(link,v).
synw(link,vp).
synw(linked, ved).
synw(linked, ven).
synw(linking, n).
synw(linking, ving).
synw(links, vp).
synw(mediate,v).
synw (mediate, vp).
synw (mediated, ved).
synw (mediated, ven).
synw(mediates, vp).
synw (mediating, n).
synw(mediating, ving).
synw (mediation, n).
synw(methylate, vp).
synw(methylate, v ).
synw (methylated, ved ).
synw(methylated, ven ).
synw(methylates, vp).
synw (methylating, n ).
synw (methylating, ving ).
synw (methylation, n).
synw(modification, n).
synw(modified, ved).
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synw(modified, ven).
synw(modifies, Vp).
synw (modify, v).
ayow(modify, vp).
eynw(modifying,n).
synw(modifying, ving).
synw(mutate, v).
synw(mutate, Vp).
synw(mutated, ved).
synw (mutated, ven).
synw (mutates, vp).
synw (mutating, n):
synw(mutating, ving).
synw (mutation, n).
synw(overexpress, v).
synw (overexpress, vp).
synw (overexpressed, ved).
synw (overexpressed, ven).
EYRW (OVEZEXPIÉBEB, VP).
evnw (overexpressing, n).
eynw (overexpressing, ving).
synw(overexpression, n).
synw(pair,v).
synw(pair, vp).
synw(paired, ved).
synw(paired, ven).
synw(pairing,n).
synw(pairing, Ving).
synw(pairs, vp).
synw(phosphorylate,n).
synw(phosphorylate,vp).
synw(phosphorylated, ved).
synw(phosphorylated, ven).
synw(phosphorylates, vp).
synw(phosphorylating,n).
synw(phosphorylating, ving).
synw(phosphorylation, n).
synw(promote, v).
synw(promote, vp).
gynw(promoted, ved).
aynw(promoted, ven).
synw(promotes, vp).
synw(promoting, n).
```

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synw (promoting, ving).
 synw(promotion,n).
 synw (prompt, n).
 synw(prompt, v).
 synw (prompt, vp).
 synw(prompted, ved).
 synw(prompted, ven).
 synw(prompting.n).
 synw(prompting, ving). .
 synw(prompts, vp).
 synw(react, v).
 synw(react, vp).
 synw(reacted, ved).
 synw(reacted, ven).
 Bynw(reacting, n).
 synw{reacting, ving}.
 synw (reaction, n).
 synw (reacts, vp).
 synw(requlate, v).
 synw(regulate, vp).
 synw(requlated, ved).
 synw(requlated, ven).
 synw(regulates.vp).
 synw (regulating, n).
 synw(regulating, ving).
 synw(regulation, n).
 synw(release,n).
 synw(releage, v).
 synw(release, vp).
 synw(released, ved).
 synw (released, ven).
 synw(releases, vp).
 synw(releasing, n).
 synw (releasing, ving).
 synw(removal,n).
 synw(remove, v).
 synw(remove, vp).
 synw(removed, ved).
 synw (removed, ven).
 synw (removes, vp).
. aynw(removing,n).
 synw(removing, ving).
 synw(replace, v).
```

```
synw(replace, Vp).
synw(replaced, ved).
synw(replaced, ven).
synw(replacement,n).
eynw(replaces, vp).
synw(replacing,n).
synw (replacing, ving).
synw(repress, Vp).
synw(repress, v).
synw(repressed, ved).
synw(repressed, ven).
synw (repressee, vp).
synw(repressing,n).
synw(repressing, ving).
synw(repression, n).
synw (require, v).
synw (require, vp).
synw(required, ved).
synw(required, ven).
synw (requirement, n).
eymw(requires, vp).
gynw(requiring,n).
synw(requiring, ving).
synw(restrain, vp).
synw(restrain,v).
synw(restrained, ved).
synw(restrained, ven).
synw(restraining,n).
eynw(restraining, ving).
synw(restrains, vp).
synw(restraint, n).
synw(sensitization, n).
synw(sensitize, vp).
synw(sensitize, v).
synw(sensitized, ved).
synw(sensitized, ven).
synw(sensitizes, vp).
synw (sensitizing, n).
synw(sensitizing, ving).
synw(separate, v).
synw(separate, vp).
synw(separated, ved).
synw(separated, ven).
```

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aynw(aeparates, vp).
synw(separating,n).
synw(separating, ving).
synw(separation, n).
synw(sever, v).
synw(sever, vp).
synw(severance,n).
synw(severed, ved).
synw(severed, ven).
synw(severing.n).
synw(severing, ving).
synw(severs, vp).
synw(signal, v).
synw(signal, vp).
synw(signaled, ved).
synw(signaled, ved).
synw(signaled, ven).
synw(signaling,n).
synw(signaling, ving).
synw(signale, vp).
synw(split,n).
synw(split,v).
synw(split, ved).
synw(split, ven).
synw(split,vp).
synw(splits,vp).
synw(splitting,n).
synw(splitting, ving) .
synw(stimulate,v).
synw(stimulate, vp).
eynw(stimulated, ved).
synw(stimulated, ven).
synw(stimulates, vp).
synw(stimulating,n).
synw(stimulating, ving).
synw(stimulation, n).
synw(substitute, v).
synw(substitute, vp).
synw(substituted, ved).
synw(substituted, ven).
eyow(substitutes, vp).
synw (substituting, n).
synw (substituting, ving).
```

```
synw(substitution, π).
synw{suppress, Vp}.
aynw(suppress, V).
synw (suppressed, ved).
synw(suppressed, ven).
synw(suppresses, vp).
synw(suppressing,n).
synw(suppressing, ving).
synw(suppression,n ).
synw(tie,n).
synw(tie,v).
synw(tie, vp).
synw(tied, ved).
synw(tied, ven)
synw(ties,vp).
synw(transcribe, v).
synw(transcribe, vp).
synw(transcribed, ved).
synw(transcribed, ven).
aynw(transcribes, vp).
synw(transcribing,n).
synw(transcribing, ving).
synw(transcription,n).
synw(tying,n).
synw(tying, ving).
synw(ubiquitinization, n).
synw(ubiquitinize, v).
synw(ubiquitinize, vp).
aynw(ubiquitinized, ved).
synw(ubiquitinized, ven).
synw (ubiquitinizea, vp).
synw (ubiquitinizing.n).
eynw{ubiquitinizing,ving}.
synw (urge, n).
synw (urge, v).
synw (urge, vp) .
synw (urged, ved).
synw (urged, ven).
synw (urges, vp) .
synw(urging,n).
synw(urging, ving).
% the following are verbs connected with complexes
synw(form, v). .
```

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```
synw(form, vp).
synw(forms, vp).
synw(formed, ved).
synw(formed, ven).
synw (forming, n).
synw(formation,n).
synw(assemble, v).
aynw(assemble, vp).
synw(assembles, vp).
synw(assembled, ved).
eynw(assembled, ven).
synw(assembling,n).
synw (assembly, n).
synw{dissassemble,v}.
synw(dissassemble,vp).
synw(dissassembles, vp).
synw{diseassembled, ved}.
synw(dissassembled, ven).
synw(diseaseembling,n).
synw(diseaseembly,n).
synw(diseociate, v).
synw(dissociate, vp).
synw(dissociates, vp).
synw(dissociated.ved).
synw(dissociated, ven).
aynw(dissociating,n).
aynw(dissociation,n).
synw(recruit, v).
synw(recruit, vp).
synw(recruits, vp).
synw(recruited, ved).
synw{recruited, ven).
synw{recruiting,n}.
synw {recruitment, n).
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WO 00/63697 PCT/DS00/10302

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% lexsemact.pat
% revised March 17, 2000
            SEMANTIC LEXICON OF ACTIONS
For genomics - the grammar tests for semantic and syntactic cate
% separately for action type of categories; for substances the lex
% entries are the same as in the medical area
% action type phrases have two entries: a semantic entry and a syn
tactic entry
% This lexicon contains the semantic entries for words and phrases
% semp is a lexical entry for phrasal lexicon
% semp(+Word1,+Sem,+Wordlist,+Targetform,+Features)
% semp specifies a semantic lexical definition for the genomics li
terature
% semp is equivalent to the predicate "phrase" in the medical area
% semp: Wordl is first word of phrase, Sem is semantic category
% semp: Wordlist is list of words in phrase, Targetform is output
% semp: Features is a list of 2 elements or the atom "def" represe
nting defaul
% semp: Features 1st element is rev or nrev meaning reversed or no
t reversed
% semp: Features 2nd element is a # specifying number of arguments
for action
% semp: Features - def is equivalent to a list = [nrev,2]
% in case action has 1 argument, use [1, ]
&semw is a lexical entry for single word
% semw(+Word, +Sem, +Targetform, +Features)
% semw: the arguments are the same as for semp except there is no
Wordlist
***
:- multifile (semp/5).
:- multifile (semw/4).
semp (account, cause, [account, for], cause, [def]).
pemp (accounted, cause, [accounted, for], cause, [def]).
```

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semp(accounting, cause, [accounting, for], cause, [def]).
semp(accounts, cause, [accounts, for], cause, [def]).
semp(add, attach, [add, up], attach, [def]).
semp(added, attach, [added, up], attach, [def]).
semp(adds, attach, [adds, up], attach, [def]).
gemp(are, cause,[are,a,meane,of, producing),cause,[def]).
semp(are, cause, [are, due, to], cause, [2, rev]).
semp(as, cause, [as, a, result, of], cause, [2, rev]).
semp(attributable, cause, [attributable, to], cause, [2, rev)).
semp(attributed, cause, [attributed, to], cause, [2, rev]).
semp (based, cause, [based, on], cause, [2, rev]).
semp(based,cause,[based,upon],cause,[2,rev]).
semp(because, cause, [because, of], cause, [2, rev]).
semp(convey, signal, [conveys,a, signal], signal, [def]).
semp(conveyed, signal, (conveyed, a, signal), signal, (def)).
semp(conveying, signal, [conveying, a. signal], signal, [def]).
gemp(conveys, signal, [conveys,a, signal],signal, [def]).
semp(dissociate, release, [dissociate, from], release, [def]).
semp(dissociated, release, [dissociated, from], release, [def]).
semp(dissociates, release, [dissociates, from], release,[def]).
semp{dissociation, release, [dissociation, from], release, [def]).
semp(down, signal, [down, '-', regulate], eignal, [def]).
                                                           % <u>ಗಿ ಡೆಂ</u>wn-
regulates B
                   A --> B
semp(down, signal, [down, '-', regulated), signal, [def]).
                                                                A down
-regulates B
                    A --> B
semp(down, signal, [down, '-', regulates], signal, [def]).
                                                                A down
                     A --> B
-requiates B
semp(down, signal, [down, '-', regulation], signal, [def]).
                                                                A dow
                    A --> B
n-requiates B
semp(due, cause, [due, to, the, fact, that], cause, [2, rev]).
semp(due, cause, [due, to], cause, [2, rev]).
semp(form, attach, [form, complex], attach, [def]).
semp(formation, attach, [formation, of, complex], attach, [def]).
semp(formed, attach, [formed, complex], attach, [def]).
semp(forms, attach, [forms, complex], attach, [def]).
semp(had, cause,[had,an,active,role,in],cause,[def]).
semp(has, cause, [has,an,active, role,in), cause, [def]).
semp(have, cause, [have, an, active, role, in], cause, [def]).
semp(is, cause, [is,a,means,of, producing], cause, [def] }.
semp(is,cause,[is,due,to],cause,(2,rev)).
semp(functions, inactivate, (functions, as, a, negative, regulator, of), i
nactivate, [def]).
semp(function, inactivate, [function, as, a, negative, regulator, of], ina
```

```
ctivate,[def]}.
semp(lead, cause, [lead,to], cause,[def]).
semp(lead, causel, [lead, to], cause, [def]).
semp(leading, cause, [leading.to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leads, cause, [leads,to], cause, [def]).
semp(leads, cause1, (leads, to), cause, [def]).
semp(led,cause, [led,to],cause, [def]).
semp(may, cause, [may, be, responsible, for), cause, [def]).
semp(mediate, signal, {mediate, a, signal), signal, [def]).
                                                                 ŝΑ
mediates a signal to B
semp(mediated, signal, [mediated, a, signal], signal, [def]).
                                                                   ş
A mediates a signal to B
semp(mediates, signal, [mediates, a, signal], signal, [def]).
A mediates a signal to B
semp(mediation, signal, [mediation.of, a, signal], signal, [def]).
    %A mediates a signal to B
semp(n, createbond, [n,'-',acetylate],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylated],'N-acetylate', {def]}.
semp(n, createbond, [n,'-',acetylates],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylation],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acylate],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylated],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylates],'N-acylate',[def]).
semp(n, createbond, (n,'-',acylation),'N-acylate',[def]).
semp(n, createbond, [n,'-',glycosylate],'N-glycosylate',[def]).
semp{n, createbond, [n,'-',glycosylated],'N-glycosylate', [def]).
semp(n, createbond, [n,'-',glycosylates],'N-glycosylate',[def]).
semp(n, createbond, in,'-',glycosylation),'N-glycosylate',[def]).
semp (n, breakhond, [n, '-', terminal, proteolysis], 'n-terminal proteoly
sis',[def]).
semp(o, createbond, [o,'-',glycosylate], '0-glycosylate',[def]).
semp(o, createbond, [o,'-',glycosylated], 'O-glycosylate',[def]).
semp(o, createbond, [o,'-',glycosylates], '0-glycosylate', {def]).
semp(o, createbond, [o,'-',qlycosylation], '0-qlycosylate',[def]).
semp(only,time,[only,after],'only after',{2.rev]).
semp(proly1, createbond, [proly1,'-',4,'-',hydroxylate],
                   'prolyl-4-hydroxylate', [def]).
semp{prolyl, createbond, [prolyl,'-',4,'-',hydroxylated].
                     'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,"-',hydroxylates],
               'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, (prolyl,'-',4,'-',hydroxylation),
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```
'prolyl-4-hydroxylate', [def] }.
gemp(result, cause, [result, from], cause, [2, rev]).
semp(result, cause, [result, in], cause, [def]).
semp(resulted, cause, [resulted, from], cause, [2, rev]).
semp{resulted, cause, {resulted, in}, cause, [def]).
semp(resulting, cause, (resulting, from), cause, (2, rev)).
semp(resulting, cause, [resulting, in], cause, [def]).
semp(results, cause, [results, from], cause, (2, rev)).
semp(results, cause, [results, in], cause, [def]).
semp(set, release, (set, free), release , [def]).
semp(set, release, [set, free], release ,[def]).
semp(sets, release, [sets, free], release , [def]).
semp(setting, release, [setting, free], release , [def]).
semp(suppress, inactivate, [suppress, activity, of], inactivate, [
def]}.
semp(suppressed, inactivate, (suppressed, activity, of), inactivat
e, [def]).
semp(suppresses, inactivate, [suppresses, activity, of], inactivat
e, [def]).
semp(suppression, inactivate, [suppression, of, activity, of], inac
tivate, [def]).
eemp(switch, activate, [switch, on, the, activity, of], activate
, {def}}.
semp(switched, activate, [switched, on, the, activity, of],
vate, [def]).
semp(switches, activate, [switches, on, the, activity, of],
vate, [def]).
semp(up, signal, [up, '-', regulate], signal, [2, rev]). % A up-regul
ates B B --> A
semp(up, signal, [up, '-', regulated), signal, [2, rev]).
eemp(up, signal, [up, '-', regulates), signal, [2, rev]).
semp(up, signal, [up, '-', regulation], signal, [2, rev]).
semp(was, cause,[was,a,means.of, producing],cause,[def]).
вещр (was, cause, [was, due, to], cause, (2, rev]).
semp(were, cause, (were.a, means, of, producing), cause, [def] }.
semp(were, cause, [were, due, to], cause, (2, rev)).
semw(acetylate, createbond, acetylate,[def]).
semw(acetylated, createbond, acetylate,[def]).
semw(acetylates, createbond, acetylate,[def]).
semw(acetylation, createbond, acetylate, [def]).
semw(activate, activate, activate, {def}).
semw(activated, activate, activate, (def)).
semw(activates, activate, activate, (def)).
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```
semw(activation, activate, activate, [def]).
semw(add, attach, attach,[def]).
semw(added, attach, attach, [def]).
semw(addition, attach,
                         attach, [def] } .
semw{adds, attach, attach,{def}}.
semw(after,time,after,[2,rev]).
                                    % temporal relations
semw(aggregate ,attach,attach,[def]).
semw(aggregated .attach,attach,[def])..
semw(aggregates, attach, attach, [def]).
semw(aggregation ,attach,attach,[def]).
semw(arrest, inactivate, inactivate, [def]).
semw(arrested, inactivate, inactivate,[def]).
semw(arrests, inactivate, inactivate, [def]).
semw(associate, attach, attach, [def]).
semw (associated, attach, attach, [def]).
semw(associates, attach, attach, [def]).
semw(association, attach, attach, [def]).
gemw(attach, attach, attach, [def]).
semw(attached ,attach,attach,[def]).
semw(attaches, attach, attach, [def]).
semw{attachment, attach, attach, [def]}.
semw(bind, attach, attach, [def]).
semw(binding, attach, attach, [def]).
semw(binds,attach,attach,[def]).
semw(block,inactivate,inactivate,[def]).
semw(blocked,inactivate,inactivate,[def]).
semw(blocking,inactivate,inactivate,[def]).
semw(blocks,inactivate,inactivate,(def)).
semw(bound, attach, attach, [def]).
semw(break, breakbond, 'break bond',[def]).
semw(breakage, breakbond,
                            'break bond', [def]).
                          'break bond', [def]).
semw(breaks, breakbond,
semw(broke, breakbond,
                         'break bond', (def)).
semw(broken, breakbond, 'break bond', [def]). % case without break
semw {catalyzation, promote, catalyze, [def]}.
eemw(catalyze,promote,catalyze, [def]).
semw(catalyzed,promote,catalyze,[def]).
semw(catalyzes, promote, catalyze, [def]).
semw(catalyzing,promote, catalyze,[def]).
semw(cause, cause, cause, [def]).
semw(caused, cause, cause, [def]).
Bemw(causes, cause, cause, [def]).
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semw(cleavage, breakbond,
                           'break bond', [def]).
semw(cleave, breakbond,
                         'break bond', [def]).
semw(cleaved, breakbond,
                          'break bond', [def] }.
semw(cleaves, breakbond,
                          'break bond', [def] }.
semw(coimmunoprecipitate, attach, attach, [def]).
semw(coimmunoprecipitated ,attach,attach,[def]).
semw(coimmunoprecipitates, attach, attach, [def)).
semw(coimmunoprecipitation ,attach,attach,[def]).
semw(combination ,attach,attach,[def]).
semw(combine .attach.attach,[def]).
semw(combined ,attach,attach,[def]).
semw(combines, attach, attach, [def]).
semw(conjugate ,attach,attach,(def)).
semw(conjugated ,attach,attach,[def]).
semw(conjugates,
                  attach, attach, [def]).
semw(conjugation ,attach,attach,[def]).
semw(connect ,attach,attach, [def]);
semw(connected ,attach,attach,[def]).
semw(connection ,attach,attach,[def]).
semw(connects, attach, attach, [def]).
semw(constrain, inactivate, inactivate,[def]).
semw(constrained, inactivate, inactivate,[def]).
semw(constrains, inactivate, inactivate,[def]).
semw(constraint, inactivate, inactivate, [def]).
semw(coprecipitate,attach,attach,[def]).
semw(coprecipitated,attach,attach,[def]).
semw(coprecipitates, attach, attach, [def]).
semw(coprecipitation ,attach,attach,[def]).
semw(copurification ,attach,attach,(def)).
semw(copurified ,attach,attach,[def]).
semw(copurifies, attach, attach, [def]).
semw(copurify ,attach,attach,[def]).
semw(couple ,attach,attach,[def]).
semw(coupled, attach, attach, [def]).
semw(couples, attach, attach, [def]).
semw(cut, breakbond, 'break bond',[def]). % leave breakbond onl
y?
semw(cute, breakbond, 'break bond',[def]).
semw(deactivate, inactivate, inactivate,[def)).
semw(deactivated, inactivate, inactivate, [def]).
semw(deactivates, inactivate, inactivate,(def)).
semw(deactivation, inactivate, inactivate.[def]).
semw(death, process, death,[1]).
```

```
semw(demethylate, breakbond, demethylate, [def]).
semw(demethylated, breakbond, demethylate,[def]).
semw(demethylates, breakbond, demethylate, [def]).
semw(demethylation, breakbond, demethylate,[def]).
semw(dephosphorylate, breakbond.dephosphorylate.{def]).
semw(dephosphorylated, breakbond, dephosphorylate, [def]).
semw(dephosphorylates, breakbond, dephosphorylate, [def]).
gemw{dephosphorylation, breakbond,dephosphorylate,[def]].
semw(die, process, death,[1]).
semw (died, process, death, [1]).
semw(dies, process, death,[1]).
semw(disassemble, release, release, [def]).
semw(disassembled, release, release, [def]).
semw(disassembles, release, release, [def]).
semw(disappembly, release, release, [def]).
semw(discharge, release, release, [def]).
semw(discharged, release, release, [def]).
semw(discharges, release, release, [def]).
semw(disengage, release, release, [def]).
semw(disengaged, release, release, [def]).
memw(disengagement, release, release, [def]).
memw(disengages, release, release, [def]).
                         'break bond', [def]}.
semw(divide, breakbond,
semw(divided, breakbond, 'break bond', [def]).
semw(divides, breakbond, 'break bond', [def]).
semw(division, breakbond, 'break bond', [def]).
semw(dying, process, death,[1]).
semw(enhance, promote, promote, [def]).
semw(enhanced, promote, promote, [def]).
semw(enhancement,promote,promote,[def]).
semw(enhances, promote, promote, [def]).
semw(enhancing,promote,promote,[def)).
semw(express, generate, express, [def]). % can have either 1 or 2 ar
quments.
semw(expressed, generate,express,[def]).
semw(expresses, generate.express.[def]).
semw(expressing, generate,express,(def)).
semw(expression,generate,express,[def]).
semw(generate,generate,generate,[def]).
semw(generated,generate,generate,[def]).
semw(generates,generate,generate,[def]).
semw(generating,generate,generate,[def]).
semw(generation,generate,generate,[def]).
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semw(hew, breakbond, 'break bond', [def]).
semw(hewed, breakbond, 'break bond', [def]).
semw(hews, breakbond, 'break bond', [def]).
semw(hinder, inactivate, inactivate,[def]).
semw{hindered, inactivate, inactivate,[def]).
semw(hinders, inactivate, inactivate,[def]).
semw(hindrance, inactivate, inactivate, [def]).
semw(inactivate, inactivate, inactivate,[def]).
semw(inactivated, inactivate, inactivate,[def]).
semw(inactivates, inactivate, inactivate, [def]).
semw(inactivation, inactivate, inactivate,[def]).
semw(incite, activate, activate,[def]).
semw(incited, activate, activate, [def]).
semw(incitement, activate, activate, [def]).
semw(incites, activate, activate, [def]).
semw(induce, activate, activate,[def]).
semw(induced, activate, activate,[def]).
semw(induces, activate, activate, [def]).
semw(induction, activate, activate, [def]).
semw(influence, activate, activate,[def]).
semw(influenced, activate, activate,[def]).
eemw(influences, activate, activate, [def]).
eemw(influencing, activate, activate,[def]).
eemw(inhibit, inactivate, inactivate,[def]).
semw{inhibited, inactivate, inactivate,[def]).
semw(inhibition, inactivate, inactivate,[def]).
semw(inhibits, inactivate, inactivate,[def]).
semw(initiate, activate, activate, [def]).
semw(initiated, activate, sctivate, [def]).
semw(initiates, activate, activate,[def]).
semw(initiattion, activate, activate, [def]).
semw(instigate, activate, activate, [def]).
semw(instigated, activate, activate,[def]).
semw(instigates, activate, activate,[def]).
semw(instigation, activate, activate, [def]).
semw(interact, interact, interact,[def]).
semw(interacted, interact, interact, [def]).
semw{interaction, interact, interact, [def]).
semw{interactions, interact, interact,[def]).
semw{interacts, react, interact,[def]).
semw(join ,attach,attach,[def]),
semw(joined ,attach, attach,[def]).
semw(joining, attach, attach,[def]).
```

```
semw(joins, attach, attach, [def]).
semw(juncture, attach, attach,[def]).
semw(liberate, release, release, [def]).
semw(liberated, release, release, [def]).
semw(liberates, release, release, [def]).
semw(liberation, release, release, [def]).
gemw(limit, inactivate, inactivate, [def]).
memw(limitation, inactivate, inactivate,[def]).
semmy(limited, inactivate, inactivate, (def)).
semw(limits, inactivate, inactivate, [def]).
semw(link,attach,attach,[def]).
semw(linked, attach, attach, [def)).
semw(linking, attach,attach, [def]).
semw(links,attach, attach,[def]).
semw{mediate, promote, promote, [def]).
semw(mediated, promote, promote, [def]).
semw(mediates, promote, promote, [def]).
semw(mediation, promote, promote, [def]).
semw(methylate, createbond, methylate, [def]).
semw(methylated, createbond, methylate, [def]).
semw(methylates, createbond, methylate,[def]).
semw(methylation, createbond, methylate,[def]).
semw (modification, modify, modify, [def]).
semw (modified, modify, modify, [def]).
semw(modifies, modify, modify, [def]).
semw (modify, modify, modify, [def]).
semw (modifying, modify, modify, [def]).
semw (mutate, modify, mutate, [1]).
semw(mutated, modify, mutate, [1]).
semw (mutates, modify, mutate, [1]).
semw(mutating, modify, mutate, [1]).
semw(mutation, modify, mutate, (1)).
semw(overexpressed, generate,overexpress,[def]).
semw(overexpresses, generate.overexpress.(def)).
semw(overexpressing, generate, overexpress, [def]).
semw(overexpress, generate, express.[def]).
semw(overexpression,generate,overexpress,[def]).
semw(pair, attach, attach, [def]).
semw(paired, attach, attach, [def]).
semw(pairing, attach, attach, [def]).
semw(pairs, attach, attach, [def]).
semw(phosphorylate, createbond, phosphorylate, [def]).
semw(phosphorylated, createbond, phosphorylate,[def]).
```

```
semw(phosphorylates, createbond, phosphorylate,[def]).
semw(phosphorylation, createbond, phosphorylate, {def)).
semw(prec de, cause, cause,[def]).
semw(preceded, cause, cause, [def)).
semw (precedes, cause, cause, [def)).
semw (preceding, cause, cause, [def]).
semw (promote, promote, promote, (def)).
semw (promoted, promote, promote, [def]).
semw(promotes, promote, [def]).
Bemw (promotion, promote, promote, [def]).
semw(prompt, activate, activate, [def]).
semw(prompted, activate, activate, [def]).
semw(prompting, activate, activate,[def]).
semw(prompts, activate, activate,[def]).
semw(react, react, [def]).
semw{reacted, react, [def]}.
semw(reaction, react, react, [def]).
semw(reactions, react, react, [def]).
semw{reacts, react, react,[def]).
semw(regulate, signal, signal,[def]).
semw(regulated, signal, signal, [def]).
                                              % B is requlated by
    A --> B
semw (regulates, signal, signal, [def]).
semw(regulation, signal, signal, [def]).
semw(release, release, release, [def]).
semw(released, release, release,[def]).
semw(releases, release, release, [def]).
semw(removal, breakbond, 'break bond', [def]).
semw (remove, breakbond, 'break bond ', [def]).
semw(remove, breakbond, 'break bond ', [def]),
semw(removes, breakbond, 'break bond ', [def]).
semw(replace, substitute, substitute, [def]),
semw(replaced, substitute, substitute, [def]).
semw(replacement,
                   substitute, substitute, [def]).
semw(replaces, substitute, substitute, [def]).
semw(repress, inactivate, inactivate, [def]).
semw(repressed, inactivate, inactivate, [def]).
semw(represses, inactivate, inactivate, [def]).
semw(repression, inactivate, inactivate, [def]).
semw(require, cause, cause, [2, rev]).
semw(required, cause, cause, (2, rev) ).
semw(requirement, cause, cause, [2, rev]).
semw(requires, cause, cause,[2,rev] ).
```

```
semw{requiring, cause, cause, (2, rev] ). .
semw(restrain, inactivate, inactivate, [def]).
semw(restrained, inactivate, inactivate,[def]).
semw{restrains, inactivate, inactivate, {def}}.
semw(restraint, inactivate, inactivate, (def)).
semw(sensitization, activate, activate, [def]).
semw(sensitize, activate, activate, [def]).
semw(sensitized, activate, activate,[def]).
semw(sensitizes, activate, activate,[def]).
semw(separate, breakbond, 'break bond', [def]).
semw(separated, breakbond,
                            'break bond', [def]).
                            'break bond', [def]).
semw(separates, breakbond,
semw(separation, breakbond, 'break bond', [def]).
                        'break bond',[def]}.
semw(sever, breakbond,
                             'break bond', [def]).
semw(severance, breakbond,
                           'break bond', [def] }.
semw(severed, breakbond,
semw(severs, breakbond, 'break bond', [def]).
semw(signal, signal, signal, [def]).
semw(signaled, signal, signal, [def]).
semw(signaling, signal, signal, [def]).
semw(signals, signal, signal, [def]).
semw(split, breakbond, 'break bond', [def]).
semw(splits, breakbond, 'break bond', [def]).
semw(splitting, breakbond, 'break bond', [def]).
semw(stimulate, activate, activate,[def]).
semw(stimulated, activate, activate, [def]).
semw(stimulates, activate, activate, [def]).
semw(stimulation, activate, activate, [def]).
semw(aubstitute, substitute, substitute,[def]).
semw(substituted, substitute, substitute, [def]).
semw(Substitutes, substitute, substitute, [def]).
semw(substitution, substitute, substitute, [def]).
semw(suppress, inactivate, inactivate, [def]).
semw(suppressed, inactivate, inactivate, [def]).
semw(suppresses, inactivate, inactivate,[def]).
aemw(suppression, inactivate, inactivate,[def]).
semw(tie.attach.attach.[def]).
semw(tied, attach, attach, [def]).
semw(ties, attach, attach, [def]).
semw(transcribe, generate, transcribe, [def]).
semw(transcribed,generate,transcribe,[def]).
semw(transcribes,generate,transcribe,[def]).
semw(transcribing, generate, transcribe, [def]).
```

```
semw(transcription, generate, transcribe, [def]).
semw(ubiquitinize, createbond, ubiquitinize, {def]).
semw(ubiquitinize, createbond, ubiquitinize, [def]).
semw(ubiquitinized, createbond, ubiquitinize,[def]).
semw(ubiquitinizes, createbond, ubiquitinize,[def]).
semw(urge, activate, activate, [def]).
semw(orge, activate, activate,[def]).
semw(urged, activate, activate,[def]).
semw(urges, activate, activate, [def]).
semw(urging, activate, activate,(def)).
semw(form,attach,attach,[def]).
semw(forms, attach, attach, [def]).
semw(formed, attach, attach, [def]).
semw(forming, attach, attach, {def}).
semw (formation, attach, attach, [def]).
semw(assemble, attach, attach, [def]).
semw (assembles, attach, attach, [def]).
semw(assembled, attach, attach, [def]).
semw (assembling, attach, attach, [def]).
semw (assembly, attach, attach, [def]).
semw(dissassemble, release, release, [def]).
semw(dissassembles, release, release, [def)).
semw (dissassembled, release, release, [def)).
semw(dissassembling, release, release, [def]).
semw(dissassembly, release, release, [def]).
semw(dissociate, release, release, [def]).
semw(dissociates, release, release, [def]).
semw(dissociated, release, release, [def]).
semw (dissociating, release, release, [def]).
semw(dissociation, release, release, [def]).
semw (recruit, attach, attach, [def]).
semw(recruits, attach, attach, [def]).
semw (recruited, attach, attach, [def]):.
semw(recruiting,attach,attach,[def]).
eemw(recruitment,attach,attach,[def]).
```

```
t edited Genome grammer - adapted from MedLEE's grammar for use with MedLEE
% this is to be used along with the genomics lexicon of substances, actions.
    and relations.
t revised March 16, April 5, 2000
* adjusted for tagged input
:- multifile(wdef/3).
: - multifile (phrase/5).
t: terterterterterter Semantic Grammar for Genomics tterterterterterterterter
      Written by Carol Friedman for the MadLEE System
                                                                               ŧ
Ŗ.
                                                                               à.
      Queens College of the City University of New York
Y Highest Level Predicate - sem_sent - lst arg. is target structure

    2nd arg. is a list of words in sentence;

                                     - 3rd arg. is '[]'
* Target structure: a frame or set of connected frames:
          the frame describes an action or several related actions;
           an action frame is a list consisting of the symbol 'action'
           followed by the code for the action and arguments.
           The arguments are either substances or actions;
           tack substance slot consists of the name of the type of
           substance followed by the value for the substance;
           the substance slot may contain slots for several substances.
* Examples:
* Blocking of il-2 gene transcription by activated rapl.
t (action,inactivate, (protein,Rapl, [state,active]),
                     {action, transcribe, [x], [gene, interleuxin-2]]}
* The adapter protein crkl was associated with both phosphorylated obl and the *
t guanidine nucleotide-releasing factor clg.
* [action,attach,[protein,CrkL],
                 [relation, and, [protein, Cbl, [state, phosphorylated]],
                              [protein, quantidine nucleotide-releasing factor C3G,
                                                     [state,phosphorylated]]]] t
并是他们电影的自然的最后的最后的主要的主要的自然的自然的情况的是不要的意思的自然的变化的自然的自然的要求的主要的的自然的思考的自然的思想的自然的自然的自然的自然的
fail an unknown predicate
:- unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=,-=]). % same priority and type as = or ==
a snoop is generally used to find input string when using a DCG
       the input string is used for constraints
snoop(A,B,A,B).
sem_sent(P,gemlist,X) -->
        {assert (addstotal (0)) },
        sem parae (P. Semlist, X).
sem_parse(Target,Semlist) -->
        sem_patterns(P,Semlist).
sem_parss(Target,Semlist,X) -->
        sem_patterns (P.Semlist) .
        sem_endornot {P, Target, X}.
sem_parse([failure],_,X,_,_} :-
        addstotal(X).
sem_endornot(P,P,X) --> % P is target if there is an endmark
```

Appendix D

```
eem endmark.
       {addstotal(X)}. % X is number of times reached endmark
sem_endornot(_'_','_','_) :- % did not reach endmark; update count and fail
       uptotal, fail,
eem endornot(_,[failure],X,_,_) :-
       addstotal(X), * x is number of times reached
* Finding patterns
sem patterns (F, Semlist) -->
       pattern(F1,Semlist);
       morepattern (R, P2, Semlist), % connected patterns
       (getrelation(R,F1,F2,F)).
* The action pattern types are: pattern, nownactionpatt, actpatt, and 🔸

    nounactpate.

    pattern --> actionarg(Al)

             active or passive verb
             actionarg(A2).
* pattern --> nounactionpatt.
* pattern --> actpatt.
* pattern is saved in a symbol table (st); check for success/failure lst
* Case where pattern is in st and has been successful
pattern(Fmt,_) --> checkst(pattern,_,s,Fmt).
t Case where pattern is in at as a failure.
pattern(_,_) --> checkst(pattern,_,f,_}, {i, fail).
$ pattern 5: an action pattern with a nominal varb

    F$1 cleavage by swad.

* apoptosis-induced cleavage of PS2 by zDEVD.
<-- captions (7, Semilist) -->
    sneep (S0, S0) ,
   { \+ checkst(pattern,5,_,_,s0,_),
    actionchk(Semlist) },
    nounactionpatt(F)
    encop (8,8),
   ( addst (pattern, 5, s, F, 80, S)
t pattern 1: an action/substance acts on an action/substance
* the activation of rap1 inhibits the expression of 11-2
4 rapl functions as a negative regulator of tor-mediated il-2 gene
4 transcription.
pattern(F,Semlist) --> snoop(80,S0), % 30 is the input string
  { \+ checkst(pattern, 1, _, _, SO, _).
    actionchk(Semlist).
    connectchk(Semlist) ),
    actionarg [A1),
```

```
connectact (Sem, [v. vp. ved] , Target, Features) ,
     actionarg(A2),
     snoop(S,S), tending sentence list
   { member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev. Peatures),
     modlist((A2, A1, Site), Mode)),
     frame (f, action, Target, Mods),
     addst (pattern. 1, s, P, So. S)
† pattern 2: an action/substance was acted on by an action/substance
t The aggregation of bad was suppressed.
t The aggregation of bad was suppressed by the phosphorylation of jnk.
a Grb2 was associated with Cbl.
* Apoptosis-associated cleavage of endogenous PSI was blocked by the
& treatment with 2VAD.
pattern(F,Semlist) -->
     snoop($0,50), * 80 is the input string
    { \+ checket(pattern, 2, _, _, 80, _}.
      actionchk(Semliat),
      connectchk(Semlist) ),
      actionarg(A2),
      sem beterm{_},
                        * was
      connectact (Sem, [ven], Target, Features), tactivated
      opthyarg(Al),
   snoop(S,S), tending sentence list
{ (member(def, Features),
      modlist ([Al,A2,Site],Mods);
      member(rev.Features),
      modlist([A2,A1,Site],Mcds)},
      frame (F, action, Target, Mode),
      addst(pattern, 2, s, F, SO, S)
   }.
$ pattern 3: an action/substance acted on an action/substance
t bad induced phosphorylation of fyn.
* ter and cd28-mediated il-2 transcription.
pattern(F.Samlist) -->
     snoop ($0,80),
   actionchk(Semlist),
     connectchk(Semlist) },
                      % substance or basic action
     actionary(Al),
   t optdash,
     connectacts (fom, [vp, ven, ved], Target, Features), ' & 'activated'
   & optof,
     actionarg(A2), & had pattern here
     encop ($,$),
  { {member(def, Features),
     modlist([A1,A2,Site],Mods);
     member(rev.Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Moda),
     addst(pattern, 3, s, F, SO, 6)
  ] .
```

```
t pattern 4: a simple action pattern with an active verb.
 t Activated Raf-1 phosphorylates MEK-1.
 pattern (P, Semlist) -->
      snoop (90, 60),
      tcheck that sentence has an action word/phrase
    { \* checkst(pattern, 4,_,_,SD,_).
      actionchk(Semlist) },
      actpatt (F).
      snoop (S.S),
    % no more patterns - save failure
 pattern(_,_) --> addst(pattern,0,f,_), {!, fail}.
   sem_morepattern(-Rel,-P,+Semlist,+80,+5):
 4
         Rel is a relation and its value frame;
 *
         P is the remaining patterns, Semlist is the list of semantic classes
         in sentence
 % if have a series of ','s, use the relation "and" or "or* if in the mest
 t and make that the relation
morepattern(R,F,Semlist) -->
         sem_relation(R1,Mod1),
                                  trelation and modifiers
         cem patterns (F. Samlist),
         (Conj2 = and; Conj2 = or), frame(R1,rel,',',_), % R1 relation frame
            frame (R, rel, Conj2, ) * value of relation is Conj2
           R1 \= (), t where do Type, Value and Mods2 come from? frome(R1,Type,Value,Mod2), % get components of original relation
           mergemods (Mod1, Mod2, Mods),
           { Mods = (), frame(R, rel, Value, ()), !;
             fframe (R, rel, [Value | Mods], []) * make it rel connector with rel mod
             R - [rel, [Value Mode]]
           )
          λ.
         }.
 % no more findings
 morepathern([],[],_,S,S).
 t actionary is the argument of pattern
 * actionary is either a substance or a basic action
 t actionary is saved in a symbol table (at); check for success/failure lat
 * Case where actioners is in st and have been successful
 actionarg(A) --> checkst(actionarg,_,s,A).
 t Case where actionary is in st as a failure.
 actionary(_) --> checkst(actionary,_,f;_), (1, fail).
 * actionarg 1: a substance or substances
 4 Rapl, active Rapl, Cbl and Crkl
 actionarg(A) --> snoop(S0,S0), % S0 is the input string
               { \* checkst(actionarg,1,_,_,SD,_)},
                 substances(A),
                 . (2,2) goons
               { addst(actionarg,1,5,A,S0,S) }.
```

```
actionary 2: a process like apoptosis, or a disease
actionarg(A) --> snoop(SO,SO), t SD is the input string
              ( \+ checket (actionarg, 2, _,_, 80, _) ),
                processpatt(A),
                snoop ($, $),
              { addst(actionarg,2,9,8,50,8)
  }.
* actionarg 3: a nominal action pattern
% Stoposide-induced apoptosis.
t Stoposide-induced PSI cleavage by zVAD.
actionarg(A) --> snoop($0,50). t 50 is the input string
              ( \+ checket(actionarg, 3, _, _, S0, _)),
                nounactionpatt(A),
                ancop (8,8),
                (addet (actionarg, 3, a, A, SD, S)
% actionary 4: the object of the nominal action is an actionary
* Blocking of IL-2 Gene transcription by activated rapl.
actionarg(A) --> snoop(S0,S0), % S0 is the input string
                 { \+ checkst(actionarg, 4 , _, _, 50, _) },
                   action(Sem, [n, ving), Target, Features),
                    (of),
                   actionary (Al),
                   optbyagent (A2),
                   snoop (S,S),
                 { (member{def, Peatures),
                   modlist([A1,A2],Mods);
                   member (rev. Features),
                   modlist([A2,A1],Mods)),
                   frame (A, action, Target, Mods),
                   addst(actionarg, 4.s, A, SO, S)
     ).
t no more actionary - save failure ·
actionary[_) --> addst(actionary,0,f,_), {1, fail}.
& nounactionpatt is a nominal action pattern which allows for left and right
* modifiers
11-2 gene transcription mediated by ter and ed28 was inhibited by rap1.
% Activated rapt functions as a negative regulator of tor and cd-28-mediated
il 2 transcription.
nounactionpatt is saved in a symbol table (st); theck for success/failure lst
t Case where nounactionpatt is in st and has been successful
nounactionpatt(A) --> checkst(nounactionpatt,_,s,A).
* Case where nounsction path is in at as a failure.
nounactionpatt(_) --> checket(nounactionpatt,_,f,_), {1, fail}.
                                        f SD is the input string
nounactionpatt(P) --> snoop(S0,S0).
                     { \+ checkst(nounactionpatt,1 ,_,_,SB,_)},
                       actionImod [L, Sym1),
                       nounactionumit(A).
                       action mod (R, Syn2),
```

```
encop (5,8).
                    { (Synl = ved, append(R, {A), RA),
                       append(L, RA, P);
                       Gynl = ving, append(R, [A], RA).
                       L = (action, Verb, Object),
                       modliet (RA, Object, Mods).
                       frame (p, action, Verb, Mods) |,
                       addst(nounactionpatt,1,s,P,S0,S1 ).
$ no more nounactionpatt - save failure
nounactionpatt(_) --> addet(nounactionpatt,0,f,_1, (!, fail).
* the central unit of the nounactionpath is a nounactpath or a process
nounactionumit(A) --> nounactpatt(A).
nounactionumit(A) --> process(A).
& left modifiers of nounactpatt
% Evad-inhibited cleavage pf Psi
actionlmod(L, ved) --> substances(S),
                      optdach,
                      action (Sem, (ved), Target, Peatures ),
                    { frame(L, action, Target, (S)) }.
* apoptosis induced cleavage of ps2
actionlmod(L, ved) --> process(9),
                      optdash,
                      action (Sem, [ved], Target, Features ),
                    { frame {L, action, Target, [S]} }.
& apoptosis causing cleavage of Psl by Evad.
# need to invert the order of nounactpatt and action1mod
action(Sem, [ving], Target, Features).
                     { frame(L,action, Target,A) }.
actionlmod([],_) --> [].
actionrmod(R, ved) --> action(Sem, [ved], Target, Peatures),
                      byagent (A), I may have to add ving to action rmod
                   { frame(R, action, Sem, A) }.
actionrmod({),_} --> [].
% activate parses a simple action between substances expressed by an active verb
* actpart is saved in a symbol table (st); check for success/failure % % lat
* Case where actpart is in st and has been successful
actpath(F) --> checket(actpath,_,s,F).
1 Case where actpatt is in st as a failure.
actpatt(_) --> checkst(actpatt,_,f,_), {i, fail}.
* actpatt 1: substance acts on substance
PDK1 phoephorylates p70e6k at Thr229
actpatt(F) -->
    snoop(80,$0), % 80 is the input string
  { \+ checkst(actpatt,1 ,_,_,50,_)),
```

```
substances(Al),
    sem_whichrel,
                       % opt 'that'
    action (Semclass, (vp, vec) , Target, Features) ,
    propopt, % added prepopt to allow action 'to' and 'with' substance
    substances (A2),
    siteinfo(Site),
    ancop(S.S).
  { (member(def, Features),
    modlist([Al,A2,Site],Mode);
    member (rev. Peatures),
    modlist((A2,A1,Site),Mods)).
    frame (F, action, Target, Mode),
    eddst(actpatt,1 ,s,F,SD,5)
  }.
% acpatt 2:
& Substance was bound by Substance
? Substance was associated to substance.
% F can give either first or second place to the second argument;
t a byagent gets first position; prepagent gets second.
t Phosphorylated Fyn was associated with Cbl.
actpatt(F) -->
    snoop(80,80), & SD is the input string
   \+ checkst(actpatt, 2, _, _, 60, _) }.
    aubstances (A1) ,
    aem_beterm(_);
    action (Semolass, [ven], Target, Features),
    opthyorprepagent (Position, A2),
    snoop($,$),
 { (member{def, Features),
   (Position=second, modlist([Al,A2,Site),Mods);
    Position= first, modlist([AZ,Al,Site),Mode));
    member (rev. Features),
   (Position-second, modlist([A2,A1,Site],Mods);
    Position= first, modlist([Al,A2,Site],Mods))},
    frame (F. action, Target, Mods),
    addst (actpatt, 2, e, F, SD, S)
 1.
* no more actpatt - save failure
actpatt(_) --> addst(actpatt,0,f,_), {!, fail).

    nounactpatt parass a simple action between substances expressed by a nominal

% verb
I nounactpatt is saved in a symbol table (st); chack for success/failure 1st
t Case where nounactpatt is in st and have been successful
nounactpatt(Fmt) --> checkst(nounactpatt, ,s,Fmt).
* Case where nounactpatt is in st as a failure.
nounactpatt(_) --> checket(nounactpatt,_,f,_), {!, fail}.
* nounactpatt 1:
* Jok phosphorylation of Had
nounautpatt(P) -->
    snoop(S0,S0), % $0 is the input string
```

```
( \* checkat (nounactpatt,1,_._,50,_) ),
    substances (Al),
    {aminoacidtest(A1)}.
    optdash,
    action(Samclass, [a], Target, Features),
    ofobject (A2),
    siteinfo(Site),
    snoop (S,S),
   { (member (def, Features) ,
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (P, action, Target, Model,
     addst (nounactpatt, 1, s, F, S0, S)
   }.
* nounactpatt 2: the binding of substance and substance
* association of Pyn and Cb1.
the reason for having this as a separate pattern is to
t prevent 'Fym and Cbl' from being parsed together as substances
nounactpatt(F) -->
    snoop(S0,S0), % 60 is the input string
 { \+ checkst(noumactpatt,2 ,_,_,90,_) },
    action(attach, [ving,n], Target, Features),
    ofobject1(A1),
    andobject (A2),
 Y siteinfo($$te),
    snoop(S,S),
 { modlist([A1,A2,Site],Mods),
    frame (P, action, Target, Mods),
    addet (nounactpatt, 2, s, F, S0, S)
   ì
% nounactpatt 3:
t The cleavage of protein by substance.
* Association of phosphorylated Byn with Cbl
* Tyrosine phosphorylation of Cbl by kinase
t optbyorprepagent determines the order of arguments; byagent is placed first;
t prepagent is placed second
nounactpatt(F) -->
   snoop(S0,S0), % SO is the input string
    { \+ checket(nounactpatt, 3 , _ , _, so, _) },
    actionof(F),
    encop (5,3),
  { addst {nounactpatt,3 ,e,9,50,8) }.
actionof(F) -->
    siteinfo(Site).
    action (Semclass, [ving, n], Target, Features),
    optofobject (A1),
    opthyorprepagent (Position, AZ),
    snoop(8,5),
  { (member (def, Features).
    (Position=second, modlist([A1,A2,Site],Mods);
     Position= first, modlist([A2,A1,Site],Mods));
     member (rev. Features),
```

```
{Position-second, modlist([AZ,A1,Site],Mods);
     Position= first, modlist([A1,A2,Site],Mode))),
     frame (F, action, Target, Mods)
  ].
% noumactpatt 4:
t Fyn association with Cbl.
nounactpatt(P) -->
    ancop(50,50), a SD is the imput string
  { \* checkst(nounactpatt,4,_,_,S0,_) }.
    substances (A1),
    action (Semplass, (ving.n), Target, Peatures).
    withobject(A2),
  % siteinfo(Site),
    encop (S, S) ,
 { modlist([A1,A2,Site],Nods),
    frame (F, action, Target, Mode),
    addst (nounactpatt, 4, 8, P, 80, 8)
 }.
aminoacidtest(X) :- X \= [aminoacid]_].
% nounactpatt %:
% IL-2 gene transcription
* Chl phosphorylation [by substance or action]
nounactpatt(F) -->
    snoop ($0,90), t so is the input string
    \+ checkst(nounactpatt,5 ,_,_,E0,_) },
    substances (AZ),
    optdash,
    action (Semclass, {n], Target, Features),
    optbyagent(Al),
 siteinfo(Site),
    encop (9.9),
 { (member(def, Features).
    modlist ([Al, A2, Site], Mods);
    member(rev,Features),
    modlist([A2,A1,Site],Mode)),
    frame (P, action, Target, Mode),
    addet (nounactpatt, 5 , s, F, SO, S)
 } -
% nounactpatt 6:
* fyn-col association.
nounactpatt(F) -->
    snoop (80,80), & 80 is the input string
    \+ checkst(nounactpatt.6 ,_,_,S0,_) ),
   'substances(Al),
    optdash,
    substances (A2),
    action (Semclass, [n, ving], Target, Features),
 * siteinfo(Site).
    enoop (8,8),
  { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Model),
    addst (nounactpatt, 6, 8, F, S0, S1
  }.
```

```
% nounactpatt 7:
t Col phosphorylated by fyn.
nounactpatt(F) -->
    snoop(SO,SO), % SO is the input string
    { \+ checkst(nounactpatt,7 ,_,_,50,_)},
    substances (A1),
    action (Semclass, [ven], Target, Features),
    [by).
    substances (A2),
 * siteinfo($1te).
    ancop($,$).
 ŧ
             { (member(def, Peatures),
    { modlist([A2,A1,Site],Mods],
             member (rev. Peatures),
              modlist([A1,A2,Site].Mods)),
      frame (F, action, Target, Mods),
      addst (nounactpatt, 7, s, F, S0, 6)
    }.
* no more nounactpatt - save failure
nounactpatt(_) --> addst(nounactpatt,0,f,_), {i, fail}.
connectact (Sem, Syn, Target, Features) -->
      action(Sem, Syn, Target, Peatures),
     (member(Sem, [cause, causel, activate, inactivate, signal, substitute, promote])).
connectacts (Sem, Syn, Target, Features) -->
      connectact (Sem, Syn, Target, Features) .
Y aminoacid like tyrosine : ex.: tyrosine Cbl phosphorylation
% at position 201 Thr
siteinfo(S) --> aminoacid(A),
                  {frame(S, site, [A], [])} .
aiteinfo(8)
                 sitepreps, % 'in', 'at'
                position(S).
miteinfo([)) --> [].
Bitepreps
             --> prepterm(in,_).
sitepreps
              --> prepterm{at,_},
position(8) --> (position),
                sem_integerterm(I),
                { frame (S, site, I, (1) }.
The definitions of actions refer to the lexicons lexsymact.pl and lexistact.pl
Sem is the semantic class; Syn is the syntactic class
% F is the target
t oneaction was added for use with moreaction to allow parsing of conjoined
* actions
Ontaction(activate, Syn, F, Ftatures)
                                        --> activateterm(Syn, F, Fcatures), { i }.
oneaction(attach, Syn, P. Features)
                                        --> attachterm(Syn, F, Features), {|}.
oneaction(breakbond, Syn, F, Features)
                                       --> breakbondterm(Syn,F,Features),{!}.
```

```
oneaction(creatchood, Syn, F, Features)
                                        --> createbondterm(Sym, P, Features), (1).
oneaction(inactivate, Syn, F, Features)
                                        --> inactivateterm(Sym, P, Features), (!).
                                         --> reactterm(Syn, F, Features), (!).
oneaction (react, Sym, F, Features)
                                         --> releaseterm(Syn, F, Features), (!).
oneaction[release, 6yn, F, Features]
                                         --> signalterm(Syn, F, Features), {!}.
oneaction(signal, Sym, F, Features)
                                        --> substituteterm(Syn, F, Features), {! }.
oneaction(substitute, Syn, F, Features)
                                        --> transcribeterm(Syn, F, Features), {!}.
oneaction(transcribe, Syn, F, Features)
                                         --> promoteterm(Syn,F,Features),(!).
oneaction (promote, Syn, F, Peatures)
oneaction(generate,Syn,F,Features)
                                         --> generateterm(Syn, F, Features), {!}.
                                           causeterm(Syn, P, Features), (!).
oneaction(cause, Syn, P. Features)
action(activate, Syn, F, Features)
                                     --> activateterm(Syn, Al, Paatures),
                            moreaction(Conj, Args),
                            {Conj - [],F =A1;
                           Conj(=[], mergemods([[action,A1]],Args,Actions),
                           frame (F1, relation, Conj, Actions), F = {F1}}.
action(attach, Syn, F, Features)
                                     --> attachterm(Syn,A1 ,Features),
                           moreaction(Conj, Args),
                            {Conj = (), F - Al};
                            Conj\=(], mergemods{[[action, A1]], Args, Actions},
                            frame (F1, relation, Conj, Actions), F = [F1]).
                                    --> breakbondtarm(Syn,F,Features),
action(breakbond, Sym, F, Features)
                           moreaction(Conj.Args),
                            (Conj = {},F =A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                           frame (F1, relation, Conj, Actions), F + [F1]}.
action(creatchond, Syn, F. Features) --> creatsbondterm(Syn, F. Features),
                           moreaction (Conj, Args),
                            {Conj = [], F = A1;
                           Conj\=[], mergemods([[action,A1]],Args,Actions),
                           frame (F1, relation, Conj. Actions), F = \{F2\}.
sction(inactivate,Syn,F,Features) --> inactivateterm(Syn,F,Features),
                           moreaction(Conj,Arga),
                            \{Conj = \{\}, F = A\};
                           Conj\=[], mergemods([[action, Al]], Args, Actions),
                            frame(F1, relation, Conj. Actions). F = [F1].
                                     --> reactterm(Sym, F, Features),
action(react, Sym, F, Features)
                           moreaction(Conj,Args),
                            \{Conj - [], F = A1;
                           Conj\=[], mergemods{[[action,Al]],Args,Actions),
                           frame [F1, relation, Conj, Actions), F - [F1]}.
                                     --> releaseterm(Syn, F, Fratures),
action(release, Syn, F, Features)
                           moreaction (Conj.Args).
                            \{Conj = [], F = A1;
                           Conj\=[]; mergemods([[action, Al]], Args, Actions),
                           frame (Fi, relation, Conj, Actions), F = [F1] ).
                                    --> signalcorm(Syn,F,Features),
action (signal, Syn, F, Peatures)
                           moreaction(Conj, Args),
                           {Conj = [], F =A1;
                           Conj\=[], mergemode([[action,Al]],Args,Actions),
                           frame (F1, relation, Conj, Actions), P - [F1]).
action(substitute, Syn, 8, Features) --> substituteterm(Syn, 6, Features),
                           moreaction(Conj,Args),
                            (Conj = [],F.=Al;
                           Conj\-[], mergemods([[action, A1]], Arge, Actions).
                           frame(F1, relation, Conj. Actions), F = {F1}}.
```

action(transcribe,Syn,F,Features) --> transcribeterm(Syn,F,Features),

```
moreaction(Conj.Args),
                            (Conj = [],F =Al;
                            Conj\=[], Margemods([[action, A1]], Args, Actions),
                            frame (F1, relation, Conj, Actions). F = [F1]).
 action(promote, 6ym, F, Features)
                                     --> promoteterm(Syn, F. Features),
                            moreaction(Conj, Args),
                            {Conj = [], F =Al;
                            Conj\=[], mergemods(([action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]}.
action (generate, Syn, F. Features)
                                    --> generateterm($yn,F,F&atures),
                            moreaction(Conj, Args),
                            {Conj = [].F =A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F - [F1] }.
 action(cause, Syn, F, Features)
                                   --> causeterm(Sym, P. Features).
                            mareaction(Conj, Args).
                            \{Conj = (), R = A1;
                            Conj\=[], mergemods(([action,Ai]],Args,Actions),
                            frame(F1,relation, Conj,Actions), F = [F1]).
% binds, phosphorylates and activates
moreaction(Conj,Args) --> sem_conjrest(Conjl),
                            oneaction (9em, Syn, A, Features),
                            moreaction(Conj2, Alist),
                           [Conj2 = [], Alist=[],Conj=Conj1, Args = [[action,A]];
                            Conj2 = [], Conj = Conj2,
                            addmod([action, A), Alist, Args; }.
moreaction([],[],$,$).
passiveconnect (Sem, [ven] . Target , Features) -->
                   sem beterm(),
                  connectact (Sem, [ven], Target, Peatures).
processpatt(A) --> disease(A).
processpatt (A) --> process (A) .
opthyorprepagent(first,A) --> byagent(A).
opthyorprepagent(second, A) --> prepagent(A).
opthyorprepagent(first,A) --> [], {A = x}.
byprprepagent(first,A) --> byagent(A).
byorprepagent (second. A) --> prepagent (A) .
optbyagent(A) --> byagent(A).
optbyzgent(A) \longrightarrow [], \{A = [x]\}.
byagent(A) --> [by],
               substances (A).
byagent(A) --> [by],
                nounactionpatt(A).
prepagent(A) --> withobject(A).
prepagent(A) --> toobject(A).
% prepagent(A) --> andobject(A).
prepagent(A) --> ofobject(A).
```

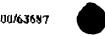
```
% optprepagent(A) --> byagent(A).
optprepagent (A) --> ofobject (A) .
optprepagent(A) --> withobject(A).
optprepagent(A) --> toobject(A) -
optprepagent(Al --> andobject(A).
optprepagent(AI --> (], {A= (x)}.
ofobject(A) --> (of),
                nounactionpatt(A).
ofobject(A) --> [of],
                substances (A).
ofobject(A) --> [of],
                actionof(A).
ofobject1(A) --> [of], substance(A). % to parse Binding of Fyn and Bad.
optofobject(A) --> ofobject(A).
optofobject([x]) --> ().
processobject(A) --> process(A). & can be expanded to nounactpatt, etc.
f optwithobject(A) --> withobject(A).
* optwithobject(A) --> [], \{A = [x]\}.
withobject(A) --> [with], substances(A).
toobject(A) --> [to], substances(A).
andobject(A) --> [and], substances(A).
prepobject (A) --> [to], substances (A).
prepchject(A) --> (with), substances(A).
optbyarg(A) --> [by],
actionarg(A).
opthyarg(A) --> substances(A).
optbyarg(A) --> [], {A = ['substance unknown']}.
prepopt --> [to].
prepopt --> [with].
prepapt --> [by].
prepapt --> [of].
prepopt --> (].
% toopt
toopt --> [to].
toopt --> {}.
% withopt
withopt --> [with] .
withopt --> [].
            ~~» ['-'].
optdash
             -->[].
optdash
optof
             --> [of].
              --> [ ].
/* optactionarg(A) --> actionarg(A).
optactionarg([]) --> (), */
optactionary(A) -->
      actionarg(A).
```

```
Y there is no further argument
optactionsrg(A) -->
    [],
    \{A - \{1\}\}.
t substances(F) --> substance(F).
t substances(F) --> substance(F1),
              moresubstances (Conj, Plist),
               (Conj - \{], Plist = [], F = P1;
¥
Ŀ.
               Conj (= [].
ŧ
             mergemods (P1, Plist, Args).
                  frame (F, relation, Conj. Args)
$ substances(F) --> substanceswithmods(F).
} substances(A) -->
                  proteins (A).
* aubewithmode.txt
$ substances is saved in a symbol table (st);
t check for success/failure lat
Case where substances is in at and has been successful
substances(Pmt) --> checkst(substances,_,s,Fmt).
t Case where substance is in st as a failure.
substances(_) --> checkst(substances,_,f,_), {!, fail}.
aubatancea(P) -->
        encop ($0,$0);
      { \* checkst {aubstances, 1, 8, _, 60, _) },
        1mode(Lmods). % left modifiers
        (several substances ([relation, Conj, First [Rest]), % conjoined substances
        rmods(Rmods), % right modifiers
* create list of lists containing distributed mods. of substances
      ( distributesubs (Dist, (First | Rest), Lmcds, Rmods),
* check Lmods - "no" F1 or F2 should be changed to no F1 and no F2
        fixecnj(Lmods,[rel,Conj],{rel,C2}),
       teplice([Conj,Dist],F)
        frame(F, relation, C2, Dist)};
* substances and modifiers without conjunction
        substance (D1),
        rmods(Rmods),
        [D1 = [Type1, Substance1 ModsD1],
        delete(ModsDi, [], ModsD2),
        append([Lmods, Rmods], WodsD2, Allmods1),
        delete(Allmods1, [], Allmods2),
        frame(F, Type1, Substance1, Alimods2))),
        snoop($,$).
       {addst(substances, 1, e, F, SD, S)}.
/* substances(8) --> snoop($0,$0),
                  {\+ chackst(substances, 3 .s, _, 50, _)},
                   complex(F).
                  \{addst(substances, 3, s, F, 80, 8)\}.
t no more substances - save failure
substances(_) --> addst(substances,0,f,_), {!, fail).
```

```
severalsubstances(F) --> substance(Pl),
                         moresubstances(Conj, Plist),
                      { Corf = [], Plist = [], F = Pl ;
                         conj \= [].
                         addmod(Pl, Plist, Argal,
                         frame (F, relation, Conj. Args)
                       }.
Y ' X, Y, and 2'
moresubstances (Conj.Args) --> sem_conjrest (Conj1),
                           substance (P1),
                           moresubstances (Conj2, Plist),
                         { Conj2 = [[, Plist = [], Conj = Conj1, Args = [Pl];
                           conj2 \= [] .Conj2\= /, Conj = Conj2.
                           addmod(Pl,Plist,Arge)
t to allow for substances with modifiers
moreaubstances(Conjl, Args) --> sem_conjrest(Conjl),
                               substances (Args) , { i } .
moresubstances([],[]] --> []. % no conjunction
* distributesubs
* distributes left mode and right mode over list of findings creating
t list of lists of findings with mode
distributesubs([),[],_,_) :- 1.
distributesubs (Dist, [D1 [Tail], Lmods, Rmods) :-
        distributesubs (Dist2, Tail, Lmods, Rmods), %distributed for remainder
        D1 = [Type1, Substance1 [ModsD1],
        append ([Lmods, Rmods), ModsD1, Allmods1),
        delete(Allmods1,[],Allmods2).
        frame (D, Typel, Substancel, Allmods2),

    append({D}, Dist2, Dist). t Combine findings to get list of findings

lmods(A) --> stateterm(F),
           {frame(A, state, F, [])}.
lmods([]) --> sem_measure(_).
lmods[[]) --> (].
rmods([]) --> (].
stateterm(F) --> acclex(state, F).
for past participle of createbond and breakbond actions, the target
tis the word. ex.: phosphorylated, dephosphorylated, methylated
stateterm(F) -->
            snoop(SO,SO), & get the initial string
            createbondterm([van], _._},
            {so = [8]_]}. *get the first word of the string
stateterm(F) -->
            snoop(90,80), % get the initial string
            breakbondterm([ven], _,_},
            (SO = [P[]]. *get the first word of the string
* may have to add attachterm for 'bound'
```



```
Taken from MedLRE grammar to handle '3 cm'
sem measure(M) -->
                   sem premeasure.
                   Sem_quantityterm(N);
                   optdash,
                   sem_measureterm(Unit),
                 { frame(M, measure, (N, Unit], []) }.
& complex predicates added November 8, 1999
% CrkL-C3G complex
% ras: raf-1 association
% ras: raf-1 complexes
% shc-grb2-sos
₹ TCR/CD3 complex
% p/CAP-p/CIP-CBP/p300-8RC-1 complex
Ras:Ref-1 complexes
complex(C) -->
                 proteins(P),
                  {P = [A,B]_J,A = {], B = {]},}
                  optcomplexword,
                 t a complex of NFAT4 with calcineurin
complex(C)
                  complexword,
             -->
                  complexarg(A),
                   {frame(c, complex, [A], [])}.
complexarg(A) --> [of], proteins(A).
complexarg(A) --> [between], proteins(A).
% a complex between MyD88, TRAK-2, and the IL-1Rs
complexarg(A) --> action(contain), proteins(A).
* Complexes containing BOB.1/OBF.1 and Oct proteins
proteins (P)
             --> protein(A),
                 moreproteins(P1),
                 {(A\={}; append((A),P1,P})}.
moreproteins (A) --> proteinconnector,
                   proteins(A).
moraproteins([]) --> [].
proteinconnector **> ['-'].
proteinconnector --> ['/'].
proteinconnector --> [';'].
* connector -->
                  (','].
                            taken out not to conflict with relation in
                   [and].
% connector -->
                                                              moresubstances
proteinconnector(C) --> [with].
optconnector -->
                   proteinconnector.
optconnector -->
                   [] -
complexword --> {complex}.
complexword --> [complexes].
complexword -->
                 ['signaling complexes'].
optcomplexword
                  --> complexword.
optcomplexword
                  ~-> [].
substance(A) --> protein(A).
```

```
substance(A) --> cell(A).
substance(A) --> species(A).
substance(A) --> structure(A).
substance(A) --> domain(A).
substance(A) --> genm(A).
substance(A) --> geneorprotein(A).
substance(A) --> aminoacid(A).
substance(A) --> smallmolecule(A).
substance(A) --> matter(A).
substance(A) - -> proteinsits(A).
substance(A) --> disease(A).
                                         a this will be modified later
substance(A) --> complex(A).
protein(A) -->
    proteinterm(P),
    {frame(A, protein, P, ())}.
complex(A) -->
    complexterm(P),
    {frame(A, complex, P, []) }.
cell(A| -->
    cellterm(P),
    \{frame(A, cell, P, [])\}.
species(A) -->
    speciesterm(P),
    {frame(A.species,P,[])}.
structure(A) -->
    structureterm(P),
    {frame(A, structure, P, [])}.
domain(A) -->
    domainterm(P),
    {frame {A; domain, P, [] | }.
gene (A) -->
    geneterm(P),
    {frame(A,gene,P,[])}.
geneorgrotein(A) -->
    gpterm(P),
    ίxΙ,
    \{(X = gene, frame(A, gene, P, []);
      X = protein, frame(A, protein, P, [1]);
      X\= gene, X \= protein, frame(A, geneorprotein, P, [1})).
aminoacid(A) -->
    aminoacidterm(P),
    {frame(A, aminoacid, P, {))}.
smallmolecule(A) -->
    smallmoleculeterm(P),
     {frame(A, 'small molecule', P, ())}.
matter(A) -->
```

```
matterterm(P),
    {frame (A, substance, P, []) }.
proteinsite(A) -->
    proteinsiteterm(P),
    {frame(A, 'protein site', p, [])}.
discase(A) -->
    diseaseterm(P).
    {frame(A, disease, P, [])}.
process(A) -->
     processterm(Syn, F, Features),
     {frame(A, process, F,[)),!}.
process(A) -->
     processterm(P),
     (frame(A, process, P, {)}.)
% terminals
proteinterm(F)
                       --> acclex{protein,F).
complexterm(F)
                      --> acclex (complex.F) .
                       --> acclex(c#11, P).
cellterm(F)
speciesterm(F)
                       --> acclex(species,F).
atructureterm(F)
                       --> acclex(structure, F).
domainterm(f)
                       --> acclex(domain,F).
                       --> acclex(gene.F).
geneterm(F)
                       --> acclex(gp, f).
gpterm(P)
aminoacidterm(F)
                      --> acclex(aminoacid,F).
smallmoleculeterm(F) ---> acclex(smallmolecule, P).
matterterm(F)
                      --> acclex(substance, P).
probeinsiteterm(F)
                      --> acclex(proteinsite,F).
diseaseterm(F)
                      --> acclex(disease,F).
processterm(F)
                      --> acclex(process, ?).
* action(activate,Sym,F,Pestures) --> activateterm(Sym,F,Pestures).
activateterm(Syn,F,Features) --> acclexes(activate, Syn,F,Features).
                               --> accless(attach, Syn, P, Features).
attachterm(Syn, F, Peatures)
breakbondterm(Byn, F, Peatures) --> acclexes(breakbond, Syn, F, Features).
createbondterm(Syn,F,Features) --> acclexes(createbond, Syn,F,Features).
inactivateterm(Syn, F. features) --> acclexes(inactivate, Syn, F. Features).
                              --> acclexss(react, Syn,F,Peatures).
reactterm(Syn, F, Features)
                               --> acclesss(release, 6ym, F, Features).
releaseterm (Byn, F, Features)
Bignalterm (Syn., F. Features)
                              --> acclexss(signal, Syn, F, Features).
substituteterm(Sym,F,Features) --> acclexes(substitute, Sym,F,Features).
transcribeterm {Syn, F, Features } -- > acclexes (transcribe, Syn, F, Features).
                              --> acclexss (promote, Syn, . Features).
promoteterm (Syn. F, Features)
                               --> acclexes(process, Sym, F, Peatures).
processterm(Syn, F, Features)
generateterm(Syn, F, Features) --> acclexes (generate, Syn, F, Features).
causeterm(Sym, F, Features)
                               --> acclexes(cause, Syn, F, Features).
4 Semilist contains a phrase which is an action
actionchk(Semlist) :-
       intersect (Semlist, (attach, cause, createbond, breakbond, activate,
                  inactivate, substitute, transcribe, express, promote, signal)).
% Semlist contains a phrase which is a connector action
```





```
电多标准分类作类类形式电影等作的语言 医皮肤生生的 美名的学生的大学的名词复数电子的大流光彩电影的多种交流技术系统的重要的等于的名词复数的重要的工程等的
                    Genome sections: ends here
* relations are connected by conjunctions, or
k
            certain 'conn' prepositions.
* Taken from MedLEE grammar to handle connectives that are conjunctions
Ł
            Ex: "severe markings, possibly from tuberculosis"
sem_relation(F,[)) -->
                       * relation and modifiers
        жет_соппаршис,
        sem_certainty([],C,rel);
        prepterm (P, conn),
        \{frame(F,rel,P,C)\}.
        tplice([[rel,P],C],R).
            Ex: "markings, swelling", "markings and swelling"
sem_relation(R,[]) --> sem_conjrcl(R),
                       выт сонтарилс.
           "density may represent known tumor"
    'markings, and swelling"
sem conjrel(F) -->
       Bem_commapuse,
       sem_conjterm(Conj),
       {frame{F, rel, Conj, []}}.
aem_conjrest(Conj) -->
                          * restricted conj, has not sem_relation_showopt
        sem commapunc,
        eem conjterm(Conj).
t "markings, swelling"
Bem_conjrest(',') -->
      ancop (S0, S0),
        вет соттарило,
      encop(8,6),
       {$0 \- $}.
* Treatment of Verbs from MedLER's Grammar
             form of "be"
sem_auxvarb(B) --> sem beterm(B).
             form of "do"
sem auxverb(B) --> sem doterm(B).
             form of "have"
sem_auxverb(B) --> sem_haveterm(B).
sem_recrel --> prepterm(in,_).
sem_recrel --> prepterm(to, ).
t "is not"
sem_auxrel(V) --> sem_auxverb(_),
                sem_negterm(V).
sem_auxrel(V) --> sem_auxverb(V).
Left modifiers of findings include negation, quantity, certainty, degree, and
                                    change type modifiers
```

```
sem_integer(W) --> [W], [integer(W)].
sem integer (W) --> integerterm (W).
sem_timeunit(T) --> sem_timeunitterm(T).
t From MedLBE grammar . "lasting 2 days", "for 2 days", "times 2 days"
gem duration(F) -->
       sem_durpreps,
        sem_premeasure, tabout
        eem timemeasure(T),
        sem_durationmod, topt. - "in duration"
        \{frame (P, duration, [T], [])\}.
Bem_duration([],3,5).
sem_durpreps -->{times].
sem_durpreps -->
    prepterm(for, ).
sem_durpreps -->[lasting,for].
sem_durpreps -->[lasting].
sem durpreps -->[lasted.for].
sem_durpreps -->[lasted].
sem durationmod -->
         sem_aposts, topt. - "'s"
        [duration].
sem_durationmod --> [in], [duration].
eem durationmod --> [].
sem_aposts --> ['''], [s].
sem_apost --> [].
% sem_frequency taken From MedL62'* grammar
% "two times", "times two", "two times a/per week", "two times daily"
sem_frequency(F) -->
        sem_freqterm(F1);
                             ಕ್ಷಿಂದ≎೯೫
        sem_freqterm(F2),
                            % "a day"
        {frame(M, unitval, (F1, F2), []),
         frame(F, frequency, [M], []) }.
sem_frequency(F) -->
        sem freqterm(M), % "gid", "daily"
        {frame(&, Erequency, M, [])).
% "2 times",
sem_frequency[F} -->
        sem_premeasure,
        aem_quantityterm(M);
        sam_times,
      \{frame [P, frequency, [M], (]\}\}.
₹ °times 2"
sem_frequency(Q) -->
        sem_times,
        sem_quantityterm(Q1);
        {frame {Q, frequency, Q1, []]}.
sem_frequency(F) -->
        [q], sem_quantityterm(Q),
             sem_timewrit(T),
        {frame [F, frequency, [unitval, [Q,T]], [])}.
```



```
sem frequency(F) --> Bom_eachevery,
                     Bem_quantityterm(Q);
                     sem_timeunit(T);
                     (frame {P, frequency, [unitval, [Q, T, every]], []]}.
#em_frequency(Q) -->

* "second*

        sem ordinal (0),
        sem_timeopt.
        [frame (Q, frequency, O, []) }.
sem_frequency([],8,9).
sem_timeopt --> [time].
sem_timeopt --> [].
sam_cachevery --> [each].
sem_eachevery ... [every].
sem_times-->(times).
sem_times-->(x).
% Taken from MedLEE's grammar
negation modifier - "no" as in "no cardiomegaly"
sem negation(f) -->
        sam_negterm(N),
        {frame(F,neg,N,[])}.
* negation not present
sem negation((),$0,80).
t Taken from MedLEB's grammar
* quantity modifier - "two" as in "two masses"
eem_quantity(P) -->
       encop(SD,96),
       { \+ checkst{scm_dates,1,s,_,80,_) }, % not a legitimate date
       sem quantityterm (Q),
                                  * "2 or 3", "2 to 3"
       sem quantityrmod(_);
                                  % rule out '2 mm*
       (\+ next_wordunit($0),
        frame(P,quantity,Q,[])
sem_quantity([],SD,SO).
sem commapunc([', '[S], 6).
sem_commapunc(6,5).
aem_conjterm(C)
                    --- acclex(conj,C).
dotarm(D)
                    --> acclex(vdo,D).
sem_endmark([.|S],S).
sem_endmark([; |S],S).
sem freqterm(F)
                    --> acclex(freq.f).
sem haveterm(H)
                    --> acclex(vhave, H).
integerterm(I)
                    --> acclex(integer,I(.
                    --> acclex(unit,M).
sem measureterm(M)
                    --> acclex (med, M).
sam_medterm(M)
sem_negterm(N)
                    --> acclex(neg,N).
prepterm (P,C)
                    --> acclex(p, [P.C]).
sem_timeunitterm(T) --> acclex(timeunit,T).
```

```
WO 00/63687
                                                               PCT/U800/10302
V lexog - adapted from MedLEE lexicon
***************** CLOSED WORD CATEGORY LEXICON $24488544844485344244
******
                        NEGATIONS
                                    $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
:-unknown(_,fail).
:-multifile(wdef/3).
wdef [cannot, neg, no].
wdef (neither, neg, no).
vácí (never, neg, no).
wdef (no, neg, no) .
wdef (non, neg, no).
vátí (nont, neg, no).
wdef (not, neg, no).
wdef (nothing, neg, no).
89889998998888888
                        wdef['&',comj,and}.
wdef('/',comj,or).
wdef('-',grammar,'-'}.
wdef('+',conj,and).
wdef(although,conj,and).
wdef (and, conj, and).
wdef (as.conj.and).
wdef(because,conj,and).
wdef(but,conj,and).
wdef(',',conj,',').
wdef (except, conj, no).
% twdeE(if,grammar,if).
wdef {minue,conj,no}.
wdef(nor,conj,no).
wdsf{or,conj,or}.
wdef(that,grammar,that).
wdef (though, conj, and).
wdef (thru, conj, and).
woet (verses, conj.or).
wdef(versus,conj,or),
wdef(vs,conj,or).
wdef (when, grammar, when).
wdef(where, grammar, where).
wdef(whereas,conj,and),
wdef (which, grammar, which).
wdef(while,conf,and).
wdef (who, grammar, who).
wdef(yet,conj,and).
```

wdef(above,ploc,above).

```
wdef(at,p,[at,ncomn]). .
wdaf(atop,p,[on,nconn]).
wdef (before.ploc.before) .
wdef(before,tprep,before).
wdef(behind.ploc.behind).
wdef (below, ploc, below).
wdef(between,ploc,between).
wdef (beyond, ploc. beyond) .
wdef(by,ploc, near).
wdef (despite, p. [with, conn]).
wdef (during, p. [during, conn] | .
wdef (during, tprep, during).
wdef (encasing, ploc, encasing).
wdef (extending,p, [in,nconn]).
wdefifollowing.p, [after,conn]).
wdef (following, tprsp, after).
wdef(for,p,[for,ncoun]).
wdef(from,p,[from,conn)).
wd#f(in,p,[in,nconn]).
wdef(including,p,[with,comn]).
wdef (into, p. (in, nconn)).
wdef(involving,p.[of,nconn]).
wdef (next, tprep, next).
wdef(occupying,p,(in,aconn)).
wdef \{on, p, [on, nconn]\}.
wdef(of,p,[of,nconn]).
wdef(over,ploc,oyer).
wdaf (overlie, ploc, over).
wdef(overlied,ploc.over).
wdef(overlies,ploc,over).
wdsf(overlying,ploc,over).
wdef (prior, tprep, before).
wdef (near, ploc, near).
wdef (radiating, ploc, radiating).
wdef (regarding, p, [about, nconn]).
                                    * 'Youghly 6 mm'
wdef (roughly, grammar, roughly).
wdef(since,p,[since,conn]).
wdef [since, status, subsequent].
wdef (through, p, [in, nconn] ).
wdef (throughout, p, [in, nconn]).
wdef(to,p,(to,nconn)).
wdef(toward,p,[to,nconn]).
wdef(towards,p,[during,conn]).
wdef (under, ploc, below) .
woef (undermeath, ploc, below) .
wdef(until,tprep,until).
wdef (up, grammar, up).
wdef(upon,p,[on,nconn]).
wdef(via,p,[with,conn]).
wdef(with,p,[with,conn]).
wdef (within, p, [in, conn]).
wdef (without, p, [no, conn]).
*wdef(without, nag, no).
wdsf{'%', unit, percent}.
```

```
wdef (cc, unit, cc).
wdef(centimeter,unit,cm).
wdef (centimeters, unit, cm),
wdef(cm, unit,cm).
wdef(degrees, unit, degree).
wdef (gm, unit, gram).
wdef (gms, unit.gram).
wdef (gram, unit, gram).
wdef(grame, unit, gram).
wdef (kg, unit, kilogram).
wdef (kilo, unit, kilogram).
wdef{kilogram, unit, kilogram}.
wdef(kilograms,unit,kilograms),
wdef (liter, unit, liter).
wdef (liters, unit, liter).
wdef (microgram, unit, microgram).
wdef (micrograms, unit, microgram).
wdef(milliliter,unit,ml).
wdef(milliliters, unit, ml).
wdef(milligram, unit, mg).
wdef(milligrams, unit, mg).
wdef(milliseconds,unit,millisecond).
wdef(millivolts, unit, millivolt).
wdef(ml,unit,ml).
wdef(millimeter,unit,mm).
wdef(millimeters, unit, mm).
wdef(mm, unit, mm).
wdef(oss,unit,ounce).
wdef(percent, unit, percent).
wdef(half,integer,'one half').
wdef{semi, quantity, semi}.
wdef (ii, integer, 2).
wdef{iii,integer,3).
wdef(vi,integer,4).
wdef(v,integer,5).
wdef (vi, integer, 5).
wdef(vii,integer,7).
wdef(viii,integer, 0).
wdef(ix, integer, 9).
wdef(xii,integer,12).
wdef(xiii,integer,13).
wdef(one,integer,1).
wdef(two,integer,2).
wdef(double, guantity, double).
wdef(three,integer,3).
wdef(four.integer.4).
wdef (quadruple, guantity, quadruple).
wdef(five, integer, 5).
wdsf(six,integer,5).
wdef(sixty,integer, 60).
wdsf(seven,integer,7).
wdef{eight,integer,8}.
wdef {nine, integer, 9}.
wdef (ten, integer, 10).
wdef {eleven, integer, 11}.
wdef (twalva, integer, 12).
```

```
wdef (thirteen, integer, 13) .
wdef (fourteen, integer, 14) .
wdef(fifteen.integer, 15).
wdef(sixteen,integer,16).
wdef (seventeen, integer, 17).
wdef(aighteen,integer,18).
wdef(nineteen,integer,19).
wdef(twenty,integer,20),
wdef(thirty,integer,30).
wdef (forty, integer, 40).
wdef(fifty,integer,50).
wdef(sixty,integer,60).
wdef(seventy,integer,70).
wdef (eighty, integer, 80).
wdef(ninety, integer, 90).
wdef (hundred, integer, 100).
wdef(thousand,integer,1000).
wdef (million.integer, 1000000).
wdef (billion, integer, billion).
wdef (zero, integer, 0).
wdof {first, ointeger, 1}.
wdsf (second, pinteger, 2).
wdef(third,ointeger,3).
wdef (fourth, ointeger, 4).
wdef (fifth, ointeger, 5) .
wdef(sixth.ointeger,6).
wdef(seventh,ointsger,7).
wdef(eighth, ointeger, 8).
wdef(minth,ointeger,9).
wdef(tenth, cinteger, 10).
wdef(eleventh, cinteger, 11).
wdef(twelvth,ointeger,12).
wdef (thirteenth, ointeger, 13).
wdef (fourteenth, ointeger, 14).
wdef(fifteenth,ointeger, 15).
wdef(sixteenth, ointeger, 16).
wdef (seventeenth, ointeger, 17).
wdef (eighteenth, ointeger, 18).
wdef (ninteenth, ointeger, 19).
wdef(triple, quantity, triple).
wdef (twentieth, ointeger, 20).
wdef (thirtieth, ointeger, 30).
wief (single, quantity, 1).
wdef (solitary, quantity, 1).
wdef (frequency, grammar, frequency) .*/
wdef 🗗 .', granmar, '.') ..
.wdef(';',grammar,';').
wdef('/',grammar,'/').
wdef(':'.grammar,':').
wdef('?', certainty, 'moderate certainty').
wdef('+',certainty,'high certainty').
wdef('''', grammar,'''').
wdsf (once, freq. 1).
wdef(times, grammar, x).
```

wdef(twice,freq.2).

```
* lexicon with lex0g containing common English words adapted from lex0 of
 MedLEET
 * lexig from lext of MedLEE
 * August 23, 1999
 . CAROL FRIEDMAN
           QUEENS COLLEGE, COLUMBIA UNIVERSITY
                      · Version 3.0 4-01-00
                       Version 2.0 1-31-96
                       Version 1.0 1-5-92
 8
                       SEMANTIC LEXICON FOR CLINICAL TEXT
 ķ.
 æ
 ð
    The lexicon consists of several files:
       lexOg.pl: single word closed classes
       lexig.pl: single word - general modifier type words:
      wdef (category, target).
 *
           word - is the name of the word being categorized;
           category - is the semantic category for the word
 ٠
 ١
           target - is the canonical/standard form for the word
                      words which are synonyms should be assigned the same
 ķ
                      canonical form.
                                                                          ŧ
 ŧ
      multi-word phrases are categorized as follows:
 ķ
                                                                          ŧ
       phrase (word, category, phrase, target).
                                                                          ż
 ŧ
     Semantic Categories:
 Ł
 8
         certainty "possible"
                canonical values limited to: moderate - for possible
                                            high - for high possible
                                                                          ٠
                                            low - for low possible
 ŧ
         conj - relational operators "and", "or", which connect one finding &
 *
 ٠
                to another finding
         neg - negation "no", "not"
         quant - for quantitative information "many"
 :-unknown( ,fail) .
:-ensure_loaded([nsphrase.lex0g.lex1g.lexsamact.lexsyn.lexsub]).
```

*/

```
A definitions kept from MedLEE lexicon - lexi.pl
wdef (be, vbe, 'high certainty').
wdof (been, vbe, 'high certainty') . .
wdof(being, vbe, 'high certainty').
wdef(was, vbe, 'high certainty').
wdef(is, vbe, 'high certainty').
wdef (were, vbe, 'high certainty').
wdef(became, voertainty, 'high certainty').
wdef (become, vcertainty, 'high certainty').
wdef (becomes, vcertainty, 'high certainty').
wdef (becoming, vcertainty, 'high certainty').
                             put in action lexicon
wdef (changed, change, change).
wdef (changes, change , change) .
wdef (changing, change, change).
wdef (necessarily, certainty, 'high certainty').
wdef (necessary, vrecommend, recommended).
wdef (necessitate, vatatus, need) .
wdef (necessitated, vetatus, need).
wdef (necessitating, vstatus, need).
wdef (necessitates, vstatus, need).
wdef (need, vetatue, need) .
wdef (needed, vatatus, need).
wdef (needing, vetatus, need).
wdef (needs, vstatus, need).
```

28

```
file ml_parger.pl
:- multifile(phrase/5).
;- multifile(wdef/3).
;-unknown(_,fail).
thoad in program components - library components are part of Prolog
:- ensure_loaded((library(basics), library(not), library(lists),
   library(readin), library(strings), library(ctypes), library(readconst),
   library(date), library(listparts), library(sets),
   radrec, radpardb, useful, util, tagging, lexicon, gengram] }.
t:- initialization run.
trun :- on exception(Error, processrun, stop(Error)).
runtime_entry(start) :- processrun.
runtime_entry(abort) :- halt.
* procesa report
processrum :- process, halt.
tstop(Error) :-
    write (user error, 'Error: '), write (user error, Error), halt.
* get user supplied parameters and process report
procesa :-
get_args(Mode, Infile, Outfile, Pro, Undefs, Protocol), 1,
            (Examtype = []; % must have a domain
            process(Infile, Dutfile, Prb, Undefs)).
t open Infile (text input) and process
process(Infils, Outfile, Prb, Undefs) :-
           see (Infile), seen, see (Infile),
           on exception (Brror,
           test_genome(Outfile, Prb, Undefs),
                app_erro(_,Cutfile,Error)),
           closefiles (Dutfile, Prb, Undefa).
process(_,Outfils,_,_) :-
        app_err(_,Outfile,'Program failed').
app_err0(_,Output,Error) :-
       tell (Output) .
       write('<error>'),
       write('Prolog Error occurred: '),
       app_err(_, Output, Error).
app_errl(_,Output,Brror) :-
       tell(Output),
       write ('<error>'),
       write('Error in input: '),
       app_err(_,Output,Error).
app_err(_, Output, Error) :-
       tell(Output),
       write(Brror), write('</error>'), nl.
closefiles (Outfile, Errfile, Unfile) :-
      tell(Outfile), told,
      {Errfile = []; tell(Errfile), told),
      (Unfile = []; tell(Unfile), told(.
```

```
Argument options - get user defined arguments
% -p ProbPile (otherwise default is problem messages are not written to file)
Infile (if input is supplied by file and not standard input
* -s Section (default is impression)
* -m Mode (default is relax; the three choices are strict, relax, skip)
4 -o Outfile (if output should be file and not standard output)
t -? Provide list of default arguments
* -u Undefs (otherwise default is - undefined messages are not written
      to a file}
get_args(Mode.Infile,Outfile,Prbfile,Undefs,Protocol) :-
    unix (args [Args]),
  (Args = [], |, writesyntax;
   Args = ['?'],!, writesyntax;
   Arge - [X Rest], I.
   set_args([X|Rest), Mode, Infile, Outfile, Prbfile, Undefs, Protocol||.
writesyntax :-
     write(user_error, 'genepareer [-m Mode]'),
     nl (user_error) ,
     write(user_error,'
                                [-t Outtype] [-p Probfile] [-u Undefs]'],
     nl (user_error) ,
                                [-i Infile] [-o Outfile]'},
     write(user error,'
     nl (user_error) .
```

```
t nsphrase.pl - contains words/phrases that are ignored
nosem(both,[both]).
nosem(however,[bowever)).
nosem(stlec_tively,[selectively]).
nosem(specifically,[specifically]).
nosem(the,[the]).
nosem(a,[a]).
```

```
% file radpardb.pl
ֆ յուրe 25, 1999
† fail an unknown predicate
 :-unknown(_,fail).
:- dynamic(sentno/1).
% \sem\radpardb.pl
%parse_sentences(*Beg, -Fmt, -ParseErrors, -Undefineds, -Unsents, +6ection,
                +UserMode, +Examtype, Sentno, Outsno, Inc$no)
       Bog is list of sentences. Fmt is list of target forms,
       ParseErrors are a list of sentences which could not parse,
.
8
       Undefineds is a list of undefined words in sentence
       Unsents is a list of sentence containing undefined words
       Section is the section of the examination, UserMode is the
       parsing mode specified by user,
       Examtype is the domain (type of exam)
       Sentno is the number of the starting sentence
       Outsno is the last sentence number + 1
       IncSno is the amount that the sentence number should be increased
4
            (i.e. it is 1 when called by paree sects and 0 when in
              recovery mode)
    Each sentence is parsed independently.
parse_sentences([],(],(],(],[],_,_,_,_,_) :- !. %no more sentences
parse sentences (Beg, Fmtlist, Outfail, Outundefs, OutunSents,
               Section.UserMode.Examtype._...IncSno) :-
   got sentence(Beg,S,Rest), !,
    ( isidentifier(8), !, % ignore identifier sentences - parse remainder
     parse_sentences {Rest, Fmt1, Outfail, Outunders, OutunSents,
                Section, UserMode, Examtype, __, _, IncSno), i,
      (outputform(htext), S \= ['.'], !, IncSno \= 0. *0 means in recovery
mode
       append([[[sentence,S]]],Fmtl,Fmtlistl;
       Fmtlist = Fmtl
     % Incano = 0, 1; % on same sentence in recovery mode
     sentno(Sno), NewSentno is Sno * IncSno,
     * retract(sentno(_)), assert(sentno(NewSentno))
   t Inceno = 1, write('***'), write_list($,3, }, nl, |,
    % Incano = 0.
     preprocess(S,Bs,Undef,Semlist,strict), t bracket and check for undefineds
     parse modes (5, Bs, Semlist, Pmtl, Errors, Undef, Unsents, Section, Writefail,
                Examtype, UserMode, Inc$no), & parse first sentence
     parse sentences (Rest, Fmt2, Moreerrors, Moreundefs, MoreUnSents,
                 append(Errors, Morestrors, Qutfail),
                                           7 Combine failures
     (outputform(htext),
           (Fmt1 = [], IncSno = 0,
            Fmt2 - [], Fmtlist - Fmtl . !
```

```
append (Fmt1, Fmt2, Fmtlist)
                    % Combine targets
      append (Unsents, MoreUnSents, OuturSents), & Combine sentences
      append (Undef, Moraundefs, Outundefs)
                                                % Combine undefined words
*parse_modes(+5,+Bs,+Semlist,-Fmt,-Failures,+Undef,-Unsents,+Section,
     +WriteMessage, +Examtype, +Mode, +IncSno)
        S is original sentence; Re is sentence after lexical lookup
¥
        Semlist is list of semantic categories in sentence
ŧ
٠
        Fmt is formatted output,
        Failures is list of sentences/fragments which could not be parsed.
ŧ
        Undef are words not in lexicon, Unsents are sentences containing
f.
                undefined words
•
        Section is name of section being processed
Ł
        WriteMessage is message returned from doresult (in case doresult fails)
ŧ
        Example is domain, Mode is user specified mode
        Incomo is 0 if this is a fragment of a sentence that was already
4
                parsed - but unsuccessfully; is 1 if this is a new sentence
* Best possible - try to get the most accurate parse possible trying
% all alternative strategies in turn if peccessary
* All words in sentence are defined
parse modes (S. Br. Semlist, Fmt, Errors, [], [], Section, no, Examtype, Pmode,
              Inc) :-
      (Pmode = bpseg, Pmodemod = mode2, !; %in recovery mode
       Prode = bpseg2, Prodemod = mode2, 1;
       Pmode - bpsegl, Pmodemod - mode2, 1;
       Pmode - bpskip, ?modemod = mode4, !; %in recovery mode % in user specified parse mode - don't parse in mode 5 or keyword
       Pmode \= keyword, Pmode \= mode5.
       Pmodemod = model
       ).
      dozent (3, Bs, Semlist, Fmtl, Message, Section, _, Examtype, Pmodemod, _), !, &
strict first
      recovery(_,3,8s,Semlist,Fmt2,Massage,Errors,[],[],Section,
                  Pmode, Examtype, _), * try alternative modes if neccy
       (outputform(btext), inc \= 0, 1, append([[[sentence,S]],Fmt1,Fmt2],Fmt);
       append (Fmt1, Fmt2, Fmt)
& alternative strategies if have undefined words
parse_modes (8,8s,Semlist,Fmt,Srrors,Undef,Unsents,Section,no,Examtype,
             Pmode, Inc) :-
     Undef \= [],
     recovery(_,S,Bs,Semlist,Fmtl,yes,Errors,Undef,Unsents,Sertion,
                Pmode, Examtype, _), % try alternatives if have undefineds
      {outputform(htext), Inc\= 0, !, append![(sentence,3]],Fmt1,Pmt);
      Fint - Fmtl
     ١,
% key word strategy is fastest but least reliable;
parse modes (3, Bs, Gemlist, Fmt, Errors, Undef, Unsents, Section, no. Examtype,
             Pmode, Inc) :-
     [Pmode = keyword; Pmode = mode5
     ; Pmode - mode5},
     recovery (5, S, S, Semlist, Fmt1, yes, Errors, Undef, Unsents, Section, Pmode,
               Examtype,_),
      (outputform(btext), Inc \= 0, (, append([[sentence,5]],Fmtl,Fmt);
```

```
Fmt1 - Pmt
     ١.
† Parsing/Recovery modes
t parse_modes(+Ltvel,+s,+Bs,+Sem,-Fmt,+Failed,+Undef,+Unssats,+Section,
              +Pmode, +Examtype,_)
    Level is the recovery level of the predicate
    S is the original sentence list
ŧ
   Bs is the
Ł
    Sem is the list of semantic categories in the sentence
    Fmt is the formatted output for the sentence
    Failed is 'yes' if the pares was unsuccessful, and 'no' otherwise
   Undef is a list of words in sentence which are undefined (not in lexicon)
   Unsents are the lists of sentences/segments which could not be parsed.
   Section is the section of the report
Pmode is the user specified parse mode
  Examtype is the domain
% mode 1 is the atrictest parsing mode - the parser succeeded for the complete
         original sentence using the grammar; all words in original sentence
ŧ
         are defined in lexicon
% mode 1 - alternative not needed because parse succeeded
recovery(1, _,_,,[],no,(],Undef,Unsents,_,_,_,) :- |.
         - no alternative strategy allowed in mode 1
٠
           in case where there are no undefineds, Noparse is S
recovery(1,$,_,_,[],yes,$,[],[],_,Pmode,_,_) :-
         Pmode = strict; Pmode = model, 1.
           in case there are undefineds, Unsents is S
recovery(1,8,_,_,[],yes,Noparse,Undef,Unsents,_,Gmode,_,_l :-
        (Pmode = strict; Pmode - 'mode1'),
        Undef \= [], Ungents - S, Noparse - [], 1.
recovery(1,8,_,Semlist,[],yes,$,_,_,_,_,_) :-
* sentence contains no relev. information, don't try to recover
      \+ (subtype(finding,Semlist); subtype(time,Semlist)), |.
\+ actionchk(6emlist). % april 23, restored
% mode 4 - skip undefined words and try to parse according to mode 1
recovery (4.5._, Fmt, yes, Errors, Undef, [], Sect, Pmode, Examtype, _) := Undef \mathbb{T} = \{],
         (Pmode = bp; Pmode = mode4;
          Fmode = bpseg; Pmode = bpskip; Pmode = mode4
         ١.
         preprocess(8,Bs,_,Semlist,bpskip).
         dostat(S,Bs,Semlist,Fmt1,Message,Sect,_,Bxamtype,mode4,_), |,
         recovery{_,Bs,Bs,Samlist,Fmt2,Message,Errors,[],[],Sect,
                      bpskip, Examtype, Santnol. 1 try alternatives if neccy
           append(Fmt1,Fmt2,Fmt).
% mode 3 - try longest parsed segment; partition rest of
             sentence using mode 5 for parse mode bp
recovery(3,S,Bs,_,Fmt,yes,Errors,Undef,Unsents,Sect,Pmode,Examtype,_) :-
         % allowable modes for choosing longest segment
         (Pmode = bp; Pmode = bpakip;
         Pmode = skip; Pmode = mode3; Pmode = mode4;
         Pmode = bpseg3; Pmode = bpseg
         ١,
         (Pmode = bpskip, Pmodemod = mode4_3;

    Pmodemod = mode3

         ١.
         checkst(sem_pattern,_,s,Target,Bs,Rest), tcheck symbol table
```

```
tdooreault(Target,Pmt1,Examtype,Sect,Pmodemod,_).
           formatresult (Target, Pmodemod, Pmt1).
          {Pmode = mode3, Pmtlist = [], Errors = Rest;
          recovery (S. Rest, Rest, _, Fmtlist, yes, Errors, Undef, Unsents, Sect,
                         Pmode, Examtype, _]
          append (Fmt1, Pmtlist, Pmt).
% mode 2 segments sentence using word barrier methods. This mode is tried if
ŧ
           parse failed for original sentence/or there are undefined words
             segment sentence using word barriers
recovery(2,8,_,_,Fmt,yes,Brrors,Undef,Unsents,Sect,Pmpde,Examtype,_) :-
          (Pmode = bp: Pmode = bpskip; Pmode = mode2; Pmode = skip;
           Prode = mode2; Prode = mode1; Prode = mode4;
           Pmode = bpseg; Pmode - bpseg2;
           Pmode - bpsegl
          segmentandparse($,Fmt,Errors,Unsents,Sert,Pmode,Examtype,_),!.
* mode 5 - try to partition sentences by findings
* when a finding in sentence is found, go left until first
    modifier is found (if 2 findings are next to each other, 2nd one
    is considered the finding and lat is considered the modifier)
    Repeat searching for successive findings using this method
recovery(5,[],[],_,[],_,[],_,_,_,] := (,
recovery(5,5,Bs,_,Pmt,yes,Brrows,Undef,Unsents,Sect,
                Proble , Exambype , _ ) :-
          (Pmode = bp; Pmode = bpskip; Pmode = bpseg; Pmode = keymode;
          Pmode - modes; Pmode - negmode
         ١.
          preprocess(8,Bs1,_,_,bpskip), % skip undefined words
          actionfindingseg (Bal, Fseg, Before), 1, % get segment containing finding
           (Feeg = [], Errors - S, 1; % no finding to segment
           *Before > (), Errore = Bs, Fmtl - [], 1; t this part was tried
           preprocess(Fseg,Bseg,_,Semlist,bpskip),
dosent(Fseg,Bseg,Semlist,Fmtl,Message,Sect,_,Examtype,
                    modeS,_! * try to parse finding segment
            (Before = [], Before[ = [], Message = yes, !; % no segmenting yet -
skip beg.
            Massage = yes, Before1 = Before, !; *don't add '.'; have to skip
more
            append (Before, ['.'], Beforel)
           ١.
            [ Faeg = [], Fmt - [], !; % no finding left in sent. - don't recover
           recoverrest (Fseg. , Beforel, Fmt2, Message, Errors,
                      Sect, Newmode, Examtype, _),
            * recover remainder
            append (Fmt1, Fmt2, Fmt)
* nothing could be recovered; all input -> Brrors ; Format is []
recovery(_,Sente,_,_,[],yes,Sents,Undef,[],_,_,_,_).
 part of phrase was skipped, add period and treated skipped part as a
  sentence
t recoverrest(+Segment,+Semlist,+Before,-Fmt,+Message,-Failures,+Section,
        +Mode,+Examtype,_}
        Segment is part of sentence with a finding
```

```
Semlist is a list of semantic categories for that sentence part
÷
¥
        Before is the part of sentence before Segment
        Fmt is the format for this segment
٩
        Message is 'no' if there is no segmentle information to be recovered
¥
                 Message is 'yes' otherwise
t
         Pailures are lists of segment(c) that could not be parsed successfully
         Section is section being processed, Mode is user specified parsing mode
        Examtype is domain
recoverrest [_,_,Before,[],no,Beforel,_,_,_) :- (Before = [], Beforel = [], :; % nothing was skipped
   append(Before,['.'],Before1}
* nothing left to recover; write phrase that was skipped
recoverrest([],_,Before,[],yes,Before1,_,_,_,_) :-
   {Before - [], Before1 = [], !/
   append(Before,['.'),Beforel)
   ), 1.
% can recover partial paree
recoverrest(B*, _, Before, Fmt, yes, Errors, Sect, Pmode, Examtype, _) :-
          checkst(sam_pattern,_.s,Target,Bs,Restseg), % recover from symbol tab.
          tdoresult(Target, Fmtl, Examtype, Sect, mode5, _),
           formatreault (Target, mode5, Fmtl),
          recovery (5, Restseg, Rest, _, Fmt2, yes, Error2,
                     [],[],Sect,Pmode,Examtype,_),
          append (Fmtl, Fmt2, Fmt),
                                                 thothing skipped to add '.' to
          (Before = [], Srrors = Error2, (;
           append(Before, ['.'[Error2], Errore)
k cannot recover partial parse - skip first element and retry
t if let element is a negation semantic type, skip 2nd element instead
      Handles case where 1st element is a negation, certainty or status
        add 2nd element to unparsed sentences list (enloosed in angle brackets).
recoverrest ([X,Y | Restseg] ,_, Beforel, Fmt, yes, Errors,
                       Sect, Pmode, Examtype, _ ) :-
          foundword (X, Seml, Tar),
          ( member(Sem1, [neg, certainty, vcertainty, vconn, status, vetatus]);
            Seml > p, Tar = (\_,conn)
           % T (Mod = neg; Mod = certainty; Mod = status; Mod = vcertainty), % leave
this mod in
           preprocess([X|Restseg],Fseg0,_,_,bpskip), % skip undefined words findingseg(Fseg0,Fseg,Before2), !, % get finding seg
           {Freg = [], Errors = \{X,Y|Restseg\}, Fmt = \{\}; * no finding
            preprocess(Feeg, Basg, _, Restsem, bpskip), t skip undefined words
            dosent (Fseg, Saeg, Resteem, Fmtl, Message, Sect, _, Examtype,
                     mode5,_}, % try to parse finding segment
            recoverrest (Freg, _, (Y | Before2) , Fmt2, Message, Error2,
                      Sect, negmode, Examtype, ), % recover remainder
            (Beforel = [], Errors = Error2, );
             append(Before1,[.|Brror2],Errors)
            ١,
            append (Fmt1, Fmt2, Fmt)
           3.
    skip lst element; enclose it in brackets
recoverrest([X|Restseg],_,Before1,Fmt,yes,Errors,
                 sect,Pmode,Examtype,_) :-
           preprocess(Restasg, Pacg0, _ , _ , bpskip) ,
```

```
findingseg(Fseg0, Fseg. Refore2), 1, 3 get finding seg
          append(Beforel, [X[Before2].Before).
          (Fseg = [], Errors = (X{Restseg], Fmt = {]; % no finding
           preprocess(Fseg,Bseg,_,Resteem,bpskip),
          dosent (Fseg, Bseg, Restsem, Fmtl, Message, Sect, , Examtype,
                    modes, ), & try to parse finding segment
          recoverrest (Pasg, _, Before, Pmt2, Message, Errors,
                      Sect, Newmode, Examtype, _), % recover remainder
          append(Fint1,Fint2,Fint)
no semantic information left; return Errors
recoverrest([X|Restseg],[];Beforel,Fmt,yes,[X|Restseg],
                Sect, Pmode, Examtype, _) .
*dosent(+5,+Bs,+Semlist,-Fmtlist,+Message,+Section,+WriteMessage,+Examtype,
        +Mede )
       S is original list of words in sentence; Bs is list after lexical lookup
ŧ
       Semilat is list of semantic categories corresponding to Bs
¥
ħ
       Emtlist is list of target forms for sentence
       Message is 'yes' if the output from parser signals a failure,
ŧ
                and 'no' otherwise
ł
ŧ
       Section is section of examination being processed
       WriteMessage eignals whether an error occurred in generating target form
       Examtype is the domain, and Mode is the user specified mode of parsing
Parse sentence and returns target in nested format
% Handles case where sentence should be skipped because info is about
    family member or peripheral to patient
dosent(S,_,Semlist,(),Error,_,_,_,_, :=
  skipsentence (S, Semlist, Error), 1.
dosent (S.Bs. Semlist, Futlist, Brrormsg, Section, Writefail, Examtype, Mode, _) :-
   attemptparse (P.Ss. sentence, Semlist, Section, Atotal),
   ( P = {failure}, Errormsg = yes, Writefail = no, ! * parse failure
      P = [], Errormeq = no, Writefail = no, Pmtlist = [], ! % smpty target
      %doresult (P, Fmtlist, Examtype, Section, Mode, _),
        formatreault (P, Mode, Emtlist),
        Errormeg = no, Writefail = no, |
      Broomeg - yes, Writefail = yes, !
   ) .
*parse_sentences(Beg,Beg,[],[],_,_,_) :- !.
% attemptparee(-P,+8s,+Structure,+Semlist,*Ptype,-Total)
        P is output from parser
        Be is list of words in sentence after lexical lookup
æ
        Structure is name of structure to be parsed
        Semlist is list of semantic categories corresponding to elements in Bs
        Total is number of times parser reached sem_sent in grammar;
                 where sem_sent is highest level predicate in grammar
* don't parse if sentence consists of only '.' or ':'
attemptparse([],Be,_,_,_) :-
   Bs = ['.']; Bs = [';').
V if a template exists for whole sentence, get parse from it
```

```
attemptparss(P,Bs,sentence,_/_/_) :-
   Bs = [X, '.'], is list(X), the whole sentence is a finding
   find sem_sent(P,X), !.
t parses and retracts wellformed string table - parses sentence
attemptparse (P, Bs, sentence, Semlist, Ftype, Atotal) :-
   retractall(wfst(_,_,_,_,_)),
   retractall (addstotal { })
   sem sent(P, Semlist, Atotal, Bs, []). !.
t parses and retracts wellformed string table - parses bodypart only
attemptperse(P.Bs,bodypart,_,_,) :-
   sem bodyloc(P.Bs.()),
   retractall(wfst(_,_,_,_,_,_)}, !.
taegmentandparse(+Sentences,-Fmtlist,-Failures,-Unsent,+Section,+Mode,
        +Examtype,+Sentno)
        Sentences is list of sentence segments.
        Fmtlist consists of the formatted output for the segments
Ł
1
        Failures is the list of unparsed segments.
        Unsent is the list of segments with undefined words.
        Section is the section being processed, Mode is the user specified mode
        Examtype is the domain and Sentro is the sentence id.
segmentandparse([],[],[],[],[],_,_,_,_) :- (.
segmentandperse (Sentences, Fmtlist, Failures, UnSent, Section, Mode,
                  Examtype, Sentno) :-
     get_sentence(Sentences,S,Rest), 1. %sentence to segment
     preprocess(S.Sl._,Samlist,Mode), (,
     (Mode - modez, NewPmode - bpseg2, 1;
     Mode = mode3, NewPmode = bpseg3, !;
      NewPmode - bpseg
     ( segment1(S1,Segs,[],seg), |,
         paras_sentences (Segs, Fmt1, Fails, _, Un1, Section, New Pmode, Sxamtype,
                            Sentno, Sentno, 01, !
      ; aegment2($1,θeg$,[],seg}, ),
         parse_sentences (Segs, Fmtl, Fails, _, Unl, Section, NewPmode, Examtype,
                            Santno, Sentno, 0), |
      : segment3{S1,Segs,[},Negstatus,seg}, !,
         parae_santences(Gegs, Fmtl, Fails, _, Unl, Section, NewPmode, Examtype,
                            Sentno, Sentno, 0), i
       ? fails if cannot segment sentence; otherwise segments remainder
      segmentandparse (Rest, Pmt2, Nexterrors, NextUns, Section, Mode,
                         Examtype, Sentno),
      append (Fmt1, Fmt2, Fmtlist),
      append (Un1, NextUns, UnSent),
      append (Fails, Nexterrors, Failures), I.
toegment1(+S, -Segs, +Bcg, +Message)
        S is list of words in sentence
٤.
        Segs consists of sentence segments as separate sentences
        Beg is list of words in sentence prior to the current portion of sentence
Þ
        Mossage is 'seg' if segmenting succeeded and 'noseg' otherwise
segment1{[],[],_,noseg} :- 1.
* segment sentence at connect phrase/word or at most conjunctions
t if negation precedes, restore negation
```

```
segment1((X|Rest),['.','<cos>'|Rem],Beq,seg) :-
     \+ sem_endmark(Rest,[]), % don't asgment if at end already
     foundword(X,Sem,Target), & get semantic classification and target
     ( X = nor, append([no], Rest, Rem) = 0k to segment at nor
     :X = without, append([no],Rest,Rem) t ox to segment at without
     %;X ≈ 't', Rest = Rem
      ; Sem = neg, Reat = [Next|Rest2], t have negation; test word after
        testforconn(Next,Sem2,Target2), Rem = [X|Rest2)
     ; testforconn(X,Sem,Target), Rest = Rem
     ١.
segment1((X{Rest], [X|Newrest], Start, Seg) :-
       append(Start, (X), Beg), % part before segmentation
       segment1 (Rest, Newrest, Beg, Seg) .
testforconn(X,Sem,Target) :-
      [ Sem = p. Target = [P.comn], P\= with * segment at connective prep
      ; member(Sem, [vccnn, vshow]) - t segment at these types of verbs
      // Sem = conj, \+ member(X, [and, or, ', ', '/', as))
     1.
% segment at certain words -
segment2([],[],[],noseg) :- 1.
segment2(S,Segs,[],seg) :-
        Beg2(S,Rest,Segs),
        \+ sem endmark(Rest,[]), !.
segment2([X |Rest], [X |Newrest], [], Seg) :-
       segment2 (Rest, Newrest, (), Seg) .
seg2([X]Rest],Rest,['.','<eos>'|Rem]} :-
        member (K, [which, that, until, where, when, while, who,
         '(',')',between,whereby,after,before,prior,
         greater, ranging ]),
        Rem w Rest, !.
segment3([],[],_,_,noseg) :- !.
* segment at conjunction - if negation preceded conjunction, add
segment3((X|Rest), Rem, Bog, Wegstatus, seg) :-
       \+ sem endmark(Rest,[]), !, % already at end of mentence
        Beg3([X[Rest],Rem,Beg,Negstatus,Beg], |...
seg3([X|Rest],Rem,Beg,Negstatus,seg] :-
        wdef(X,conj,_},
       member(X,[and,or,',']),
        (nonvar(Negstatus), Rem = ('.', Negstatus Rest], : trestore negstion
        ; Rem = ['.','<eos>'[Rest], !
seg3([X|Rest],[X,'.','<eos>'|Rest],_,_,seg) :-
       foundword(X,age), !.
aeg3{[X|Rest],(X|Newrest],Start,Negstatus,Segi :-
        ( nonver(Negatatus), (; % lst neg already found - continue segmenting foundword(X,Sem,Target), !
            ( Target = no, Negstatus = X, !:
              Sem = neg, Negetatus = X, !;
              Sem \= neg, Target \= no, !
            ٦,
```

```
* file radrec.pl
% September 7, 1999
fail an unknown predicate
:-unknown(_,fail).
% same priority and type as \+
;- dynamic(domain/1).
                               * domain being processed
                               4 form of output (needed to distinguish
:- Gymamic(outputform/1).
                               t markup of text from formatting forms
                               * section for outputting results
; - dynamic(currentsect/1).
test_genome(Outfile, Brrfile, Unfile) :-
     get_inputsents([),Toklist), !, % read in and tokenize input
                        $ error condition
     (Toklist = [], !.
      app_errl(_,Outfile,'No input sent'), !
      parse_sentences(Toklist,Fmtlist,Failed,Undef,UnSent,impression,
bp,genome,_,_,0);;;
      outputresults (Fmtlist, Failed, Errfile, Undef, Unfile, UnSent, Outfile,
                    full, line, genome, 1, 0, _, exe, plain)
     λ.
outputresults[FmtlistO,Failed,Errfile,Undef,Unfile,UnSent,Outfile,
                Amount, Type, Exam, Compno, DocComp, NewCompno, Caller, Protocol) :-
      tell(Outfile),
     {Protocol = sgml, I, Op = sgml;
       Caller = server, !, Op = sgml;
        Op = plain),
      (Type - nested, ), % original output form - nested findings
        write('<nested>'), new line(Op),
         write(Fmtlist), new_line(Op), write('</nested>'),
        new line (Op), I
       ),
     (Caller = server,
      write_message(Unfile.Undef,Caller,'<undefined>','</undefined>')
      Caller = exe, Undef \= (),
      write_message(Unfile,Undef,Caller,'***** Undefined Words ******, [])
     twrite_highlight([],UnSent,Caller)
       true
      ),
     (Caller - server,
     write('<noparse>'),1,
     write_highlight (Undef, UnSent, Caller).
     write_highlight([], Failed, Caller), write('</noparae>')
     Caller - exe, Errfile \= [], Failed \= [],
     tell(Errfile),
     write('**** Sentences/Phrases Not Parsed *****), nl,
     twrite_highlight(Undet,UnSent,Caller),
     write_highlight([], Pailed, Caller)
     trus
             & no Errfile to write to
    ١,
% set args: Process options
```

```
& Argument options
8 p Probfile (Otherwise default is problem messages are not written to file)
§ -i Infile (if input is supplied by file and not standard input
n Mode (default is bp; the 6 choices are bp, model - mode5)
t -o Outfile (if output should be file and not standard output)
+ -? Provide list of default arguments
* -pr Protocol - sgml or plain {default is plain!
t -u Undefs (otherwise default is - undefined messages are not written
     to a (ile)
set args(Args, Mode, Infile, Outfile, Prbfile, Undef, Protocol) :-
      set mode(Args, Mode), set_amount(Args, Amount),
      set protocol(Args, Protocol),
      set infile(Args, Infile), set outfile(Args, Outfile),
      set_prbfile(Args, Prbfile), set_undefs(Args, Undef).
set mode(Args, Mode) :-
    (nextto('-m',M,Args); nextto(m,M,Args)), !,
   modeis(M,Mode), !.
set_mode( ,bp). * default output type
modeis(relax,mode2) :- !.
modeis(strict,model) :- !.
models(skip, mode4) :- i.
modeis(longest, mode3) :- 1.
modeis(best,bp) :- !.
modeis(model,model) :- (.
modeis(mode2,mode2) :- (.
.! -: [Eebom, Eebom] sisbom
modeis(mode4,mode4) :- !.
modela(mode5,mode5) :- ).
set_protocol(Args, Protocol) :-
    (nextto('-pr',Protocol,Args); nextto('pr',Protocol,Args));
    member (Protocol, [sgml, plain]), i.
set_protocol(_,plain).
set_undefs(Arge,Undefe) :-
   nextto('-u',Undefs,Args); nextto(u,Undefs,Args) , !. & undef file option
set_undefs{_,[]).
                  % default is no file of undefineds created
set_infile(Args,Infile) :-
   nonvar{Infile}, ); % Infile is set already
   nextto('-i', Infile, Args), !;
   nextto(i,Infile,Args), !.
set prbfile(Args,Prbfile) :-
   nextto('-p',Prbfile,Args), !; nextto(p,Prbfile,Args), !. % prob file option
set_outfile(Arge,Outfile) :-
   nonvar(Outfile), );
                        t Outfile is already set
   nextto('-o',Outfile,Args), !; nextto(o,Outfile,Args), |. * outfile option
set_outfile(_,user_output). * default is standard output
new_line(sgml).:- write('<br>'}, nl, }.
new line(server) :- write('<br>'),nl, !.
new line (exe) :- nl.
```

```
new_line(plain) :- nl. '
write_massage(_,[].exe,_,_) :- !.
write_message([],_,exe,_,) :- !.
write_message(_,[],plain,_,_} :- !.
write_message([],_,plain,_,} :-!-
write_message(File,Contents,Caller,Segmeg,Endmag) :-
   f member(Caller,[exe,plain]), tell(File), {
    true),
    write(Begmsg), new line(Caller).
   {Contents = []; write_list(Contents,1), new_line(Caller)
   (Snameg = [], (;
    write(Endmag), !, new_line(Caller)
sentend([X|_],Caller) :-
   member(X,['.',',','?']), new_line(Caller), ).
gettargets([],[]) :- !.
gettargets ([ignore|Rest], [ignore|Rest]) : 1. % possibly ignore info.
gettargets([W1|Rest],(T1|Trest]) :-
     foundword(W1,_,T1), * target for W1
     gettargets (Rest, Trest) , | .
gettargets (W, W). % not in lexicon
isneg(x) :-
    intersect (X, [no,negative, deny, 'rule out']).
writeoutsent([Mord(Rest]) :-
  write('''), write(Word), write(''''), !,
  (Word = '''', write(''''), ); true),
  (Rest \= [], write(','), !, writeoutsent(Rest), !; .
   true), 1.
```

```
This file contains predicates associated with SGML tags
  nextTag(+L,Tag,-PreTag,-PostTag) is true if
      L is the starting List
     Tag is an SGML tag; it could be a variable or instantiated already
Ł
      PreTag is portion of L preceding Tag
      PostTag is portion of L following Tag
nextTag(L, Tag, PreTag, PostTag) :-
    append(PreTag,['c',Tag,'>'|PostTag],L).
% endTag(+L,+Tag,-Pre,-Post) is true if
     L is the starting list
      Tag is the SGML end tag
¥
     Pre is the portion of 1 preceding the end of tag
     Post is the portion of L following the end of tag
endTag(L,Tag,Pre,Post) :-
    append((Pre,['s','/',Tag,'s'],Post],L).
t enclosedPart(+L, +Tag, -Enclosed) is true if
     L is the starting List; it is assumed that L is portion of some
      list that follows a begin tag - i.e. 'c', Tag L
     Tag is the 60ML tag
      Enclosed is the parties of text enclosed in tag; not including
      end tag.
enclosed, Post) :-
    endTag(L,Tag,Enclosed,Post).
```

```
% file useful of - lexical lookup and utility tools
  :-unknown(_,fail).
  :-dynamic(sentence/1).
  :- op[900, fy, (not, once]). % same priority and type as \+
  t useful.pl February 21, 1992
  t proprocess(+S, +B$1, -U, -Sem3, +Mode); preprocesses sentence to
              bracket lexical phrases and remove words/phrases in
              special db of noise words (nosem in asphrase.pl db)
 ŧ
          8 is original sentence
 ¥
          Bal is proprocessed sentence
 Ł
          U is list of undefined words in sentence
          Mode is mode of process - in akip mode undefined words are removed
           from preprocessed sentence
 preprocess(50,Bs1,U,Sem3,Mode) :- ·
                                          ₹cfnew
___checkbeg($0,$), % if beginning is 'Al' ignore
   checkphrase (5.51, Seml), % bracket all phrases in phrasal lexicon first
   checklist(S1,U1,Bs,Sem2,Mode), % check that all words are in lexicon, remove
   checklist (Bs.U. Bsl. Sem3. Mode). & check for phrases after non-sem are removed
  tappend (Seml, Sem2, Seml),
  tappend (Seml, Sem3, Semlist),
   tunion (U1, U2, U).
 t found checks if word X is defined as a single word, or if X starts a defined
 t phrase
 foundword(X) :-
 \begin{array}{c} \text{wdef}\left(X, \_, \_\right], \quad I: \\ \text{foundword}\left(K\right) \quad : = \end{array}
      semw(X,_,_,_),).
 *definition from tagged input
 foundword(X) :-
 phr(X,_,_,), ),
foundword((X|Rest)) :-
        Rest \- [].
      phrasal(X,_,[X[Rest],_), !.
 3/99 added foundword to search the new semact.pl lexicon
 * phrasal using semp was added to util.lp
 % found/2 returns semantic cat. of word
 coundword(X,Sem) :-
      wdef(X,Sem,_).
 foundword(X, Sem) :-
       ១៩៧५ (X, Sem,_,_) .
 tdefinition from tagged input
 foundword (X, Sem) :- ]
       phr (X, Sem, [],_).
 foundword([X | Rest], Sem) :-
      phrasal(X,Sem,[X|Rest],_).
 found/3 returns semantic cat, and target form
 foundword (X, Sem, Form) :-
      wdef (X, Sem, Form).
 foundword(X,Sem,Form) :-
       semw (K, Sem, Form, _) .
 Adefinition from tagged input
 foundword(X,Sem,Form, ) :-
       phr {X, Sem, [], Form}.
 foundword ([X|Rest], Sem, Form) :-
```

```
phresal(X, Sem, (X | Rest], Form),
*collectsem(+Word, -Sem): Sem is the list of semantic classes corresponding
    to Word
collectsem(Word, Sem) :-
    setof (X, foundword (Word, X), Sem).
t missing checks if a word present in a centence is defined
-: (X)pnissim
     member (X,S),
     not foundword(X).
t checkbeg(+80,-8) checks beginning of sentence; if it begins with a letter or
& number followed by a ')', that part is skipped
checkbeg((X,')'|Rest],Rest) :- |.
checkbeg(X,X).
* checks every word in a list to see if it is defined; creates
$ a new list of words not defined, and a new list of sentence
* where phrases are bracketed.
checklist([],[],[],[],[],[].
Y if X is a list it has already been identified as a phrase in phrasal lex
checklist([X Rest], Undef, Newrest, Semlist, Mode) :-
     ie_liet(X),
     chack_no_sem([X|Rest],Rest1,_],
     checklist (Restl, Undef, Newrest, Semlist, Mode), 1. % is phrase part of nosem
checklist({X|Rest],Undef,[X|Newrest],Semlist,Mode) :-
     %collectsem(X,Sem),
     is_list(X),
                 X = [W1|Tail],
    phrasal(W1,Sem,X,_),
     checklist(Rest,Undef,Newrest,Sem2,Mode) , !,
     append([Sem],Sem2,Semlist).
checklist([without|Rest], Undef, Newrest, Semlist, Mode) :-
     checklist({with,no|Rest],Undef,Newrest,Semlist,Mode).
* this problem has to be fixed in preprocessor
* check for a number with a ', ' - "11,200" and fix it
*checklist([X,',',',Y|Rest],Undef,[N|Newrest],[number|Semlist],Mode) :-
    number(X), number(Y), N is X * 1000 + Y, 1,
     checklist(Rest, Undef, Newrest, Semlist, Model, !.
t check for a literal number
                              *cfnew
checklist([X|Rest],Undef,[X|Mewrest],(number|Semlist],Mode) :-
    number(X).
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
% beginning of List is a preflx of a phrase that is a complete finding
checklist(List,Undef,(Phrase|Newrest),[cfinding|Semlist],Mode) :-
    check_sem_finding(List,Rest,Phrase).
     chacklist (Rest, Undef, Newrest, Semlist, Mode) , !.
3 beginning of List is a prefix of a phrase that is in nosemantic lexicon
checklist(List, Undaf, Newrest, Semlist, Mode) :-
    check_no_sem(List,Rest,Phrase),
     checklist (Rest, Undef, Newrest, Semlist, Mode), ).
t beginning of List is a prefix of a phrase that is in phrasel lexicon
chacklist(List,Undef,[Phrase[Newrest],Semlist,Mode) :=
    get_longest_sem(List,Rest,Phrase,Sem),
     checklist (Rest, Undef, Newrest, Sem2, Mode) , :,
    append (Sem, Sem2, Semlist).
& beginning of List is a single word that is in sementic lexicon
checklist({X|Rest], Undef,[X|Newrest],Semlist,Mode):-
```

```
collectsem(X,Sem), i,
     *foundword(X,Sem), !,
     checklist (Rest, Undef, Newrest, Sem2, Mode). !.
     append (Sem, Sem2, Semlist).
& beginning of List is an undefined word
checklist((X|Rest), Undefs, Nrest, Semlist, Mode): .
     checklist (Rest, Undef, Newrest, Semlist, Mode),
     (member(X,Undef), !; Undefs = (X|Undef), !),
     (Mode = skip, !, Nrest = Newrest;
      Mode - bpskip, |, Nrest = Newrest;
      Nrest = [X[Newrest]], !.
* if beginning is a number followed by a . followed by a non number
's skip,
         scfpew
checkphrase((X,.],(X,.],(1) :- 1.
checkphrase([X,.,Z|Rest],Y,Semlist) :-
     number(X), not(number(Z)), checkphrase(Rest,Y,Semlist), i.
t beginning of List is a prefix of a phrase that is a complete finding
t or a phrase in phrasal lexicon
checkphrase(List, (Phrase|Newrest), Semlist) :-
     (check_sem_finding(List,Rest,Phrase), Sem = {cfindingl;
      get_longest_sem(List, Rest, Phrase, Sem)
     1. 1.
     Ycheck sem(List, Rest, Phrase, Sem)), (,
     checkphrase (Rest, Newrest, Sem2) , | .
     append (Sem, Sem2, Semlist).
checkphrase([W|Rest],[W|Newrest],Semlist) :-
     checkphrase (Rest, Newsest, Semlist) .
checkphrase([],[],{]).
check_sem_finding([W]Tail],Teil,W) :-
           W = [W1|Rest], * W is bracketed already
           sem finding sent {W1, N, }.
check_sem_finding([W|Tail],Sfinal,Phrase] :-
           sem_finding_sent(W.Phrase,_),
           begsublist (Phrase, [W(Tail], Sfinal), 1.
sem_finding_sent(_,_,_) :- fail.
& check_nd_sem(+Sent,-Rest,-Phrase): removes Phrase from Sent resulting
     in Rest if Sent begins with a phrase in nosem (non-semantic list).
check no sem([W[Tail], Gfinal, Phrase] :-
           nosem(W, Phrase), tphrase beg. with W that should be removed
           begsublist (Phrase, [W Teil], S1),
           remove_comma(81,Sfinal), (. t remove ", " if it is next
tget_longest_sem(+Sent,-Rest,-Phrase,-Sem): Phrase is longest phrase that is
& a prefix of Sent; Rest is remainder and Sem is list of semantic classes
gat_longest_sem(Sent,Rest,Phrase,[Sem]) :-
        setof(X,check_sem(Sent,X),L), % set of Phrases
        maxphrase(L,[],Phrase,0). t Phrase with maximum length append(Phrase,Rest,Sent). t rest of sentence after Phrase
        foundword (Phrase, Sem) .
% check_sem(+Sent,-Rest,-Phrase,-Sem): checks if phrase beginning with
        Sent is in phrasal lexicon; Rest is the remainder of Sent after phrase
9
        Sem is the semantic class
check_sem{{W|Tail}, Rest, Phrase, Sem} :-
           phrasal (W. Sem, Phrase, _) .
           begsublist (Phrase, [M|Tail], Rest).
```

```
% file util.pl
$$$$$$$$$$$$$$$$$$$ Utility Predicates 859888$$$$$
fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [not,once]). & same priority and type as \+
;- op{700, xfx, (\-, -=)}
                               $ same priority and type as * or ==
:- dynamic(wfst/6).
: dynamic (addstotal/1).
:- dynamic(paragno/1).
:- dynamic(sectno/1).
:- dynamic(phr/4).
% wfst(+Rule,+Number,+Res,+Fmt,+60,+S): well-formed symbol table
% Dule is the name of rule; Number is the option number
        Res is a for success and f for failure
ŧ
        Fmr is the format (for successes); for failure Fmt is [)
9
        SD is the sentence position at the start of Rule
æ
        S is the sentence position when Rule has been completed
4
         add to wist
addst (Rule, Number, Res, Fmt, SO. S) :-
    \(\checkst(Rule,Number,Res,Fmc,80,8),\) $result for rule was saved already \(\checkst(Rule,Number,i,Smt,$0.8),\) $ result from different rule saved
   ( checket (Rule, _, Ros, Fmt, SO,S). & different rule produced same result
       assert (wfst (Rule, Number, i, Fmt, 60, 5));
    assert (wfst (Rule, Number, Res, Pmt, SO, S) )), 1.
addst(_,_,_,_,):- !. t always succeed
% checkst(+Rule,-Number.-Res,-Amt,+$0,-$): checks to see if rule has been saved
     in wist
checkst (Rule, Number, Res, Smt, SO, S) :-
    wfst (Rule, Number, Res, Pmt, SO, S).
t beglist (L,Y) - is Y the head of list L
beglist([X]],Y) := X = Y , !.
* aplice(+LI,-L2) : L1 is a list of lists, L2 is marged list
splice(L1, L2) :- append(L1, L2), 1.
tsplice([],(]) :- (.
*eplice([[]],[]) :- ).
\operatorname{*splice}([X],X) := \{...\}
tsplice([[][L1],L2) :- eplice(L1,L2),!..
%splice([[[]]|L1],L2) :- splice(L1,L2),!.
taplice([X [[]]],L) := splice(X,L).!.
tsplice([L1,L2],L3) :-
        append(L1,L2,L3), !.
Ł
*splice([X]L1],L2) :-
         splice(LL,L3(,
       append(X,L3,L2) , 1.
$splicerel - works with relations which have Argl,...,Aryn.
              It splices a Splicelist in each arg of relation
splicerel (Finding, Splicelist, Spliced) :-
             splice(Splicelist, Sp1),
             (Finding = [rel, X | Rest], spliceargs (Rest, Spl. Sp).
               *splice([[rel,X],Sp],Spliced),!;
```

```
append([rel,x],sp,Spliced).5;
              *splice({Finding, Spl], Spliced) ).
              append(Finding, Spl. Spliced) }.
Aspliceargs - Splices a list into each element of a list
spliceargs([],_,[]] :-i.
epliceargs ([Arg1 | Rest], Splicelist, Spliced) :-
           #splice([Arg1, Splicelist], Sarg1),
           append(Argl,Splicelist,Sargl),
           spliceargs (Rest.Splicelist.Srest),
           tsplice([[Sarg1],Srest],Spliced].
           append((Sargl), Srest, Spliced).
list([],[]).
list([x][)),X}.
list((X|L1), &2) :- list(L1, L3),
                  append([X],L3,L2), !.
% strip(L1, L2) removes extra square brackets from L
strip{{L},L}.
* B is a suffix of A and C is the difference
difflist(A,B,C) :- append(C,B,A).
% S is a sublist at beg. of L if there is a list Rest, which when appended
    to S results in L.
begsublist(5,L,Rest) :- append(S,Rest,L), ).
% checks that first element in list 9 has semantic category in Semlist
firstword([W1]_],Semlist) :-
    atom(N1), wdef(W1,Sem,_), t semantic category
    member (Sem, Semlist).
firstword([W1|_],Semlist) :-
    is_list(Wil, phrasel(W1,Sem,_,_),
    member (Sem, Semlist).
* removes phrases from first arg that are in asphrase - lexicon of non-sem.
ритезев
remove_no_sem([],[]) :- 1.
remove_no_sem([W|Tail],Sfinal) :-
           nosem(W, Phrase), *phrase beg. with W
           begsublist(Phrase, [N Tail), S1), fremove from sentence
           remove_comma($1,32), % remove "," if it is next
           remove_no_sem($2,$final), (.
remove_no_sem{[W|Tail],Sfinal} :-
           remove_no_sem(Tail,S1),
           append([W],S1,Sfinal) . !.
remove_comma([','|Tail],Tail}.
remove comma(S,S).
* remove_sem(+Sent,-WewSent): Sent is the original sentence, NewSent is
     stripped of all phrases that are defined in lexicon
remove_sem([],[]) :- (.
remove_sem(S,NewS) :-
    remove sem (Rest, NewS) / !..
Yemove_sem(8,N¢w$) :-
    chack_no_sem(S,Rest,_),
                           t phrase in sent. is in nosem list - remove it
    remove_sem (Rest, NewS) , |.
remove_sem([X[Tail],[X[NewS]] :-
    remove_sem(Tail, NewS), i. t not a phrase, process rest
* remove_words(+Sent,-NewSent): Sent is the original sentence, NewSent
   is stripped of all words that are in lexicon
```

```
remove_words{[], {]} :- [,
remove_words([X]Rest],NewRest) :-
     ( (foundword(X); number(X)).
                                     % X is defined in lexicon
       remove_words(Rest, NewRest) .!;
       remove_words(Rest,New), NewRest > [X|New), } % X is not in lexicon
*maxphrase(+ListofPhrases,+Maxin,-MaxQut,InitMaxLen) is true if
    ListofPhrase is a list of multi-word phrases,
      Maxim is phrase with maximum words so far
      MaxOut is phrase with maximum length of phrases in ListofPhrases
      InitMaxLen is length of initial phrase which is of max. length
maxphrase[[],Maxin,Maxin,_] := :. % no more phrases - maximum is same as maxim
maxphrase([P|Rest], Maxin, Maxout, InitMaxLen] :-
     length (P. Len) , & length of first phrase
     ( Len > InitNaxLen, ), maxphrase(Rest,P,Maxout,Len);
       Len c InitMaxLen, (, maxphrase (Rest, Maxin, Maxout, InitMaxLen)
     }.
titesittistesitesitesitesite lexical interface predicates trattitistististististist
Pacclex(Bem, W, SD, S) :-
    outputform(htext), !, acclex1(Sem, W, SO, S).
acclex(Sem, W, SO, S) :-
   acclex2 (Sem. W.SD, S).
acclex(Sem, W, SD, S) :-
   acclexes (Sem, Syn, Target, Features, SO, S).
P check lexicon for word or phrase, Target form is original W
acclex1(p,[P,C],[W|Rest],Rest) :-
         is list(W),
         find_sem_phrase(p, [F, C], W).
acclex1(p, [P,C], [W]S], S) :- atom(W),
                             wdef (N, p, \{P,C\}).
acclex1(Sem, [W], [W|Rest], Rest) : .
         is list (W), %if bracketed list, get Sem and Code from phrasal lexicon
         find_sem_phrase(Sem,_,W).
acclex1 (8em, W, [W|S], S) :-
                            wdef(W,Sem,_).
% check lexicon for word or phrase, Target form is taken from lexicon
*acclex8(Sem, Code, [W|Rest], Rest) :-
          is_list(W), Wif bracketed list, get Sem and Code from phrasal lexicon
          find sem phrass (Sem, Code, W).
acclex2(Sem, Code, [W|S],S):- foundword(W, Sem, Code),
                                             nonvar (Code) .
                                                               % protect against
lex. error
t find a phrase [W|Tail] in lexicon that begins with W and has category Sem
find_sem_phrass(Sem,Code, [W|Tail]) :-
         phrasal(W, Sem, [W Tail], Code); & phrase and code beg, with W
         nonvar (Code) .
t case where phrase is already bracketed, look up phrase
sem_finding_phrasel(Code,[W|Tail],Tail) :-
         is_list(N), *phrase is bracketed
         find_sem_sent(Code,W),
          nonvar (Code) .
                          *protect against lexical error
t case where phrase is already bracketed, look up phrase
sem_finding_phrase2(Code,[N{Tail),Tail) :-
         is list (W), aphrase is bracketed
```

```
find sem_sent(Code,W),
          nonvar(Code) *protect against lexical error
* Phrasal succeeds if lexicon contains phrase
phrasal (W1, Sem, Phrase, Code) :-
       phrase (W1, Sem, Phrase, Code, ). %multi-word phrase in lexicon
t added Warch15, 1999
phrasal (W1, Sem, Phrase, Code) :-
            semp (W1, Sem, Phrase, Code, Features) .
Y lexical definition from marked up imput
phrasal (W1, Sem, [W1 | Tail], Code) :-
            phr (W1, Sem, Tail, Code) .
acclexas(Sem,Syn,Target,Features,(N|S].S):-
            atom(W),
            semw (W. Sem, Target, Peatures),
            synw(W, Synclass),
            member (Synclass, Syn).
acclexes (Sem, Syn, Target, Features, [W[S], S]: -
            is list(W),
            find phrasess (W, Sem, Syn, Target, Features).
find phrasess ([W1 | Tail], Sem, Syn, Target, Features) :-
            semp (W1, Sem, [W1 | Tail], Target, Features),
            symp(W1, [W1|Tail],Symclass),
            member (Synclass, 6yn).
> lexical definition of a complete finding
find_sem sent(Code,[W|Tail)) :-
         sem_finding_sent(W,[W|Tail],Code).
listify(c,[c]) :-
         atom(C), 1.
listify(c,c) :-
          is list(C), I.
t distributes left mode and right mode over list of findings creating
t list of lists of findings with mode
distributemods([],[],_,_,_) :- |.
distributemods(Dist, [D1] Twil), Lmods, Rmods, Type) :-
       distributemods (Dist2, Tail, Lmods, Rmods, Type), % distributed for remainder
        mergemods (Lmods, Rmods, Allmods),
        frame(D, Type,D1,Allmode), tType frame with mods
        append((D).Dist2,Dist).
                                     & Combine findings to get list of findings
$ fixconj - if Leftmods has [certainty,no], and Conj = or, change Conj to and.
        no R or B = no A and no B; 'denies A.B. or C' is similar.
fixconj(Leftmods,Conj,[rel,and]) :-
        {member([certainty,no],Leftmode); member([certainty,deny],Leftmode)},
        Conj = [rel, ar].
fixconj( ,Conj,Conj).
         write_sentences/1 inputs a PROLOG list and prints out lines
         which which are English sentences. No wrapping is done.
write_sentences[{}} :- |.
write sentences([X]) :- write(X), nl. % special sentence - section name
write_sentences(['<',p,'/','>']) :-
     write(''), nl.
                           & paragraph mark
write sentences([X|Rest]) :-
        upper_first((X|Rest),(U|Rest)),
```

```
write(U), t First letter of first word made upper case
        IX = U, chkforpunct(D, Rest), !, write_terms(Rest); % no space needed
        write(' '), write terms(Rest)
         write_sentence/2 inputs a PROLOG list and prints out an English
         sentence wrapped. Idlen is the starting position of the sentence
         in the output.
ŧ
          uses libraries ctypes, basic, not
write_sentence([X[Rest],Idlen) :-
    upper first([X|Rest], [U|Rest]),
    write (U),
    name (U, LU), length (LU, L),
    (U = X, chkforpunct(U, Rest), !, write_terms(Rest, L+Idlen);
    write(' '), write_terms(Rest, L+Idlen+1)
    ١.
        write list inputs a PROLOG list and prints out a sentence like list.
ŧ
         wrapped. Idles is the starting position of the list in the output.
write_list{[X|Rest],Idlen) :-
    write(XI,
    name (K, LU), length (LU, L),
   ( chkforpunct(%, Rest), write terms(Rest, L+Idlen), !;
     write(' '), write terms(Rest, L+Idlen+1)).
twrite list(+List,+Idlan,-Idlanout)
a write_list prints out a sentence like list with wrapping if necessary.
    List is the list to be printed
    Idlen is the column position at start
    Idlenout is the column position at end
write_list((),Len,Len) :- !.
write_ligt({X|Rest},Idlen,Idlenout) :-
    acomic(X), write(X),
    name(X,LU), length(LU,L),
    (L + Idlen > 74, nl, Idlen2 = 1, !;
     Idlen2 - L + Idlen, |
  (chkforpunct(X,Rest), write_list(Rest,Idlen2,Idlenout). !;
   write(' '), write list{Rest,L+Idlen2+1,Idlenout}, !
   is_list(X), write_list(X,Idlen,Idlen2), write_list(Rest,Idlen2,Idlenout).
upper_first([X[Rest], [U|Rest]]:-
     name(X, [L[X]]).
 (is_alpha(L), Up is L - 32, !; Up = L),
 name (U, (Up[2]), L
% write_terms/1 writes out a word followed by blank, except for punctuations.
write terms([]) :- 1.
t case where X is and of sentence
write terms({X|Rest}) :-
   (X = {}^{t}, {}^{t}; X = {}^{t}; {}^{t}), \in A last word of sentence
   write(X), nl, !, write_sentences(Rest), !.
Y case where K is interior of sentence
write_terms([K|Rest]) :-
     write(X),
     (chkforpunct(X,Rest), write_terms(Rest);
```

```
write(' '), write terms(Rest)
      ), 4,
* write_terms(List, Used); writes the terms in list and counts the number
        of columns used; starts new line if 75 columns have been used
write_terms([),_) :- |.
% at end of list
write_terms([.], _} :- write('.'), nl,!.
write_terms([;],_} :- write(';'), q1,!.
X is a punctuation, don't add to final count
write_terms({X|R},Used) :-
   ( R = [], write(' '), write(x), ';
    chkforpunct(X,R),
    write(%), write_terms(R,Used), !
  ).
* X is last word in sentence
write_terms([K,.], Used):-
   pame(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Need,
    (Total =< 75, write(' '), write(K), write[.);
    Total > 75, 01, write(' '), write(X), write(.)),
   nl, !.
* X is last word in sentence
writs_terms([X,;], Used):-
   name (X, List), length (List, Len),
   Need is Len + 2,
   Total is Used + Reed,
   (Total =< 75, write(' '), write(X), write(';');</pre>
    Total > 75, nl, write(* '), write(X), write(.)),
   nl, I.
* X is followed by ','
write_terms([X,','|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Nord,
   (Total =< 75, write(' '), write(X), write(','),
    write_terms(Rest, Total);
    Total > 75, nl, write(' '}, write(X), write(','),
    New is Need - 1, write_terms(Rest, New}),
* writes blank + name of X, used is length of name+1
write_terms([X | Rest], Vsed):-
   name (X, List), length (List, Len),
   Weed is Lan + 1,
   Total is Used + Need,
   [Total =< 75, write(' '), write(X), write_terms(Rest, Total);
Total > 75, nl, write(' '), write(X), write_terms(Rest, Len)}, |.
write_terms(['X,''s'|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 3,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write("'a"),
    write terms (Rest, Total);
    Total > 75, nl, write(%), write_terms(Rest, Len)), |.
* processes sentences in Infile; writes formats to Outfile
e sentences beginning with '8' are treated as comments
testaenta(Infile,Outfile) :-
```

```
see (Infile), seen, see (Infile).
    tell(Outfile),
    readtests,
    ses (Infile), seen, told.
% reads next sentence and processes it
readtests :-
    read in (X),
    (x = end of file, !/
    \mathbf{x} = \{eoff, [\cdot, \cdot], \cdot\}
     X = \{Y^{\perp}\}_{\perp} \{Y^{\perp}\}_{\perp}
     X = ['%']_], !, readtests; % don't process comments
     preprocess (X, Bs, Undef, Semlist, skip),
    ( Undef = [],
     dosent(X,Bs,Semlist,Pmt,Messagt,impression,W,chestxray,Strict,0).
     write sentence(X,1), write(%3), nl,
     write(Fmt), nl;
     Undef \= [], write_sentence(X,1), write(Bs), nl, write(Undef|, nl),
                   & read next sentence
     readtests
Reads in all sentences from input file and creates one list of all sentences
get_inputsents(Prevlist, Toklist) :-
     read in (X),
     (X = end of file, Toklist = Prevlist, !;
      X = [eoff, '.'], Toklist = Prevlist, !;
      X = [''], Toklist = Prevlist, !:
      (last{'',X}, append(Toklist,[''],X], !;
                                                 *remove
       append(Prevlist, X, Newlist),
       get_inputsents(Newlist, Toklist)
      )).
*get sentence(+A, -B, -C)
& Gets next sentence from input list containing all sentences read in
% Don't end a sentence if "." is preceded by a number and followed by
% a number and unit measure - 1.25 cm, 1.5 cm, .5 cm
% or is followed by s "." which is part of abbreviation
% get_sentence(A,B,C) - A is list of all sentences in report.
                      - B is list containing one sentence
                      - C is remainder excluding B
* sgml tag for multi-word phrase containing '.' that is not end of sentence
get_sentence(('<',phr|Tail),Sentence,LRest) :-</pre>
        enclosedPart (Tail, phr. Retween, Rem), & Between beg. part of open phr and
close tag of phr
      attribute
      (MoreAttributes = ['>'[Phrase], TargetList = Phrase, !;
       MoreAttributes = (t,~,'"'|TargetPlus), % Target terms plus and of phr
       append(TargetList,['"','>'|Phrase],TargetPlus}, } % t attribute followed
by actual phrase
      ł,
      Phrase - [W1 Rest],
      append (Phrase, BRost, Sentence) ,
      concat atom(TargetList, Target),
      assert {phr {W1, Sem, Rest, Target}}, & assert lex def according to input
        %Phrase = [W1|PRest].
        Wabbrev(W1, [W1] PRest), Target, _),
        get_sentence(Rem, SRept, LRest), 1.
```

```
t Ignore sentence starting with 't', get next sentence
get_Bentence(['%','%'|Rest],Sent,Remainder) :-
     get_sentence(Rest,_,Rem),
     get_sentence(Ram, Sent, Remainder).
get_sentence{[X,.,Y,Z]Rest], [X,.], [Y,Z]Rest]):= Y break up "140. 3+"
     number \{X\}, number \{Y\}, x = +++, i = -4 Y belongs to +++ for new sentence
get_sentence([X,.,Y,Z{Rest],[N|SRest],LRest) :-
                                                      $ 1.5 Cm
      number(X), number(Y),
      t(wdef(Z,unit,_); Z = x),
      2 \= '+'. % break up "140. 3+"
      name(X,D1), name(.,D2), name(Y,D3), name('B+00',D4),
      append([D1,D2,D3,D4],D), name(N,D), Y put number together
      get_sentence([2|Rest], SRest, LRest).
$ common abbrev
get_Bentence{[X,. |Rest], [X|SRest], LRest| :-
                                                % abbrev ending in "."
t list of common abbreviations seen in reports should not end sentence
   member(K, [vs.dr.cm.mg]), get_sentence(Rest, $Rest, $Rest), i.
t list of start of names in reports should not end sentence
get sentence([X,. Rest],[X|SRest],LRest) :-
                                               % abbrev ending in "."
   member(X, [ms, mr, mrs, dr, st]),
   skipname (Rest.Rest0), % skip name part
   get sentence(Rest0, $Rest, LRest), !.
* more known abbreviations
get_sentence((W1|Rest),[Rep|SRest],LRest) :-
     abbrevchk([W1|Rest],_,Rem,Rep), t abbreviation
     gst_sentence(Rem, SRest, LRest), !.
% possible simple xml tag for new paragraph
get_sentence(['<',p,'/','>'|Reat],Sent,Reml :- %skip paragraph darker
   get sentance (Rest, Sent, Rem), 1.
% xml tag for sentence '<B>'
get sentence [['<',s,'>'|Tail], Sentence, Rest) :-
      enclosedPart(Tail,s,Sent,Rest),
       {last!'.', Sent), Sentence = Sent, !; %already has '.'
      append (Sent, [.], Santance)
      ), 1.-
                     tadd '.'
get sentence([. {Rest],[.],Rest) :- :. }end of a sentence
get_sentence([; Rest],[;),Rest] :- !.
t interior of sentence
get_sentencs([x|Rest],[x|SRest],LRest) :-
                       get_sentence(Rest, SRest, LRest).
get_sentence({],{],[]}.
                          % no more ≤entences
t abbrevchk(+WordList,-AbList,-RemList,-Target) is true if an abbrev is prefix
   of WordList, RemList is suffix of WordList (excluding prefix),
   Ablist is prefix consisting of abbreviation
   and Target is target form of abbreviation
abbrevchk([W1|Rest],AbList,RomList,Target) :-
     abbrev(W1,Ablist,Target,Dom). % abbrev knowledge base indexed by 1st word
     append(Ablist,Rem,[W1 Rest]), % remainder of abbrev. must be in sentence
     (Dom = general, !;
                         % abbrev. Applies to all domains
      domain (Thisrep), Dom = Thisrap, !: % abbrav, applies to this domain
      is_list(Dom), member(Thisrep,Dom) % this domain in abbrev. list
     Ι,
     ( % add back '.' to septence if it also signals end of sentence
      Rem = {}, last('.',AbList), Remlist = ['.'], | %no more words
      ; Y words that generally start a new sentence
```

```
Rem = [W2]_], last('.',AbList), member(W2,[his,her,he,she,the,this)),
        RemList = [',']Rem], !
        * # don't add '. ' back
       RemList = Rem
     1.
skipname(+Beglist,-Endlist): skips next word after "mr" or "st"
skipname([],[]] :-!.
skipname([_{Rest],Rest] :- ! ..
%get section(+Toklist,-Sents,-Rest,-Section,-Printname,Addno)
Toklist contains input list; 1st sentence should be a header;
* Sents are all sentences in section; Section is name of section
& Sentences at beg. of Toxlist are ignored until a section header is found
get_section([T|Toklist], Sents, Rest, Section, Printneme, Addno) :-
       * first sentence should be section header
      get_scatence([T|Toklist],Sentence,RToklist),
      (section_header(Sentence, Rsent, Section, Printname), % Sentence is a section
header
       append(Rsent, RToklist, RToklist2),
       get_sectionsents(RToklistZ,Sents,Rest),
       (Addno = 0, !; % testing if input begins with section header
       Addno - 1, ! , sectno (Sectno) , Newno is Sectno + 1,
       retractall(sectno()), assert(sectno(Newno))
      ; % let sentence is not a legitimate header - return []
       Section - []
       % get_section(RToklist, Sents, Rest, Section) % skip till find header
get_section([],[],[],[],[],...).
get_sectionsents([],[],[]) :-!.
get sectionsents(Toklist,Slist,Rest) :-
     ( - section_header(Bentence, _ , _ ) , twore sentences in section
       get sectionsents (RToklist, RSents, Rest),
       append (Sentence, RSenta, Slist)
       ; I the next section is a section header - return
      Rest - Toklist, Slist = []).
section_header(S,RestS,'report clinical information item'.
          'CLINICAL INFORMATION: ,') :-
    ($ = [elinical,information,':','.'], !, RestS = [];
     begaublist([clinical,information,':'],S.RestS), !,
     S = [clininfo,';','.'], Rest3 = {], | ;
     begaublist ([climinfo, ':'], 9, Rest$), |
    ١.
section header(S, RestS, 'report impression item',
           'IMPRESSION: .'] :-
   (S • [impression, ':', .], RestS = [], !;
    begaublist((impression, ':'), S, RestS), !
section_header(S,Rest,'report summary item','SUMMARY:.') :-
    8 = [summary, ': | Rest].
```

```
section header(S.Rest8, 'report description item', 'DESCRIPTION: ') :-
   (S = [description, ': '...), RestS = [], (;
    begsublist([description,':'],S,RestS), 1
   ) .
section header(S,Rest,'report diagnosis item','DISCHARGE DIAGNOSIS:.') :-
   [6 = [discharge, diagnosis, ': '|Rest] ;
    S = [final, diagnosis, ': (Rest];
    S = [principle, diagnosis, ':'|Rest]; S = [associated, diagnosis, ':'|Rest];
    S = [transfer,diagnosis,':'[Rest];
    6 = [diagnosis,'(',es,')',';'|Rest);
    S = [diagnosis,:|Rest)
   ), !.
section_header(5,Rest,'report laboratory data item(,'LAB DATA:.') :-
    S = [laboratory,data,':'|Rest), !.
section_beader($,Rost,'report medications item'.'MEDICATIONS:.') :-
    S = [madications,':'|Rest], ).
section_header(S,Rest,'report current medications item','MEDICATIONS:.') :-
    S = [current, medications, ': ' | Rest], |.
section_header(9,Rest, report discharge medications item',
        'DISCHARGE MEDICATIONS:.') :-
    S = [discharge, medications, ': '|Rest], }.
section header(9,Rest, 'report discharge disposition item',
     'DISCHARGE DISPOSITION: .') :-
    S - [discharge_disposition,':'|Rest], !.
section_header(S,Rest,'report medications on admission item',
     'MEDICATIONS: . ') :-
    8 = [medications.on,admission,':'|Rest), ).
section_header(S,Rest,'report medications on transfer iterm',
     'MEDICATIONS: . ') :-
     8 = [medications, on, transfer, ': | Rest], !.
section_header(S,Rest,'report procedure item','PROCEDURE:.') :-
  (S = [operation, ': '|Rest]; S = [procedure, ': '|Rest]
section_header(S,Rest,'report indications for procedure item','INDICATIONS:.')
  (S = [indications, for, procedure, ': '[Rest], S =
(indications, for, operation, ': ') Rest)
  ١,
   1
section_header(S,Rest,'report preoperative diagnosis item','PREOP DIAGNOSIS:.')
   S = [preoperative_diagnosis,':'|Rest], |.
saction header (8. Rest. 'report admitting diagnosis item', 'ADMITTING
DIAGNOSIS: . '):-
   S = [admitting,diagnosis,':'[Rest], !..
section_header(8,Rest, 'report postoperative diagnosis item', 'DIAGNOSIS:.') :-
   S = [postopsrative,diagnosis,':'[Rest], :.
section_header(6,Rest, 'report physical examination item',
        'PHYSICAL EXAM: .' ] :-
   S = [physical, examination, ': '|Rest], !.
section_header(S,Rest, 'report chief complaint item', 'CHIEF COMPLAINT: .'] :-
   S = [chief,complaint,':'[Rest], 1.
section_header(S,Rest,'report hospital course item','ROSPITAL COURSE:.') :-
   S = [hospital,course,': | Rest], !.
```

```
section_header(S,Rest,'report allergy item','ALLERGIES:.') :-
    S = [allergies, ': | Rest] (.
section_header(S, Rest, 'report follow up item', 'FOLLOW UP: ') :-
   S = [follow, up, ': ' | Rest], 1.
section_header(S.Rest, 'report findings item', 'FINDINGS:.') :-
   S = [findings,':'|Rest], !.
section_header(S,Rest,'report indications and findings item','FINDINGS:.'| :-
   5 = (indications, and, findings, ':' | Reet), ;.
section_header(8,Rest,'report indications and findings item','INDICATIONS:.') :-
   S = [indications, ': 'Rest], !.
section_header(5,Rest,'report provisional diagnosis item','PRELIM DIAGNOSIS:.')
   S = [provisional,diagnosis,':'|Rest), !.
section_header(S.Rest.'report review of systems item', 'REVIEW OF SYSTEMS: ') :-
   S = [review,of.systems, '; '|Rest], !.
section_header{S,Rest,'report past history item', 'PAST MEDICAL HISTORY:.') :-
   5 = [past, history, section, ': 'Rest], !.
section_header(6,Rest,'report past history item', 'PAST MEDICAL RISTORY:.') :-
   S = [psst,medical,history,':'|Rest], !,
section_header(S,Rest,'report social history item', 'SOCIAL HISTORY:,') :-
   S = [social, history, ': '| Rest], 1.
section_header(S, Rest, 'report past history item', 'PAST MEDICAL HISTORY: ') ;.

    S = [history,':'|Rest], 1.

section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:,') :-
   S = [brief, history, ': 'Rest], 1.
section_header(S.Rest, 'report history of present illness item',
          'HISTORY OF PRESENT ILLNESS: .') :-
   S = [history,of,present,illness,':'[Rest], !.
section_header(S,Rest,'report history of present illness item',
          'HISTORY OF PRESENT ILLMESS: .') :-
   S = [history.of,the.present,illness,':'|Rest], (...)
section_header(S,Rest,'report specimen item','SPECIMEN') :-
   5 - [specimen Rest], 1.
sentence consists of id number only or "." only.
isidentifier([X, .]) :-
        integer(x).
ieidentifier([%,;]) ;-
        integer(X),
isidentifier([.]) :- ). * sentence consists only of .
isidentifier(['.','4809>']) :- !.
isidentifier(['<',p,'/','>']) :- * paragraph marker sentence - update no. -
       paragno(N),
       retractali (paragno (_j),
       Newno is N + 1,
       assert (paragno (Newno)),
       retractall(senteo()),
       assert (sentho (0)).
* tripsentence is true, if sentence should be ignored.
* Skip sentences containing family info
ekipsentence([X|_}) ;-
   foundword(X, family), 1,
akipsentence((X|_)) ;-
   foundword (X, insurance), 1.
* This occurs if sentence contains
```

```
t a sequence in skips database and sentence also contains findings.
 skipsentence([X{Rest].Semlist.Error) :-
    skips([X|65eq]), & X is the beg. of subseq. in skip database
    prefix([X|Rest],[X|Sseq]), & sentence contains subseq.
    (subtype(_,Semlist), & sentence contains information to be extracted
     Error - no; * don't try to segment
     Error • yes}, !.
                        % treat sentence as error and try to segment.
 skipsentence([ | Rest], Semlist, Error] :-
    Bkipsentence(Rest, Semlist, Error).
 findingseg(+S,~Pseg,-Begseg): partitions sentence
         S is the sentence; Begseg is the segment preceding the
 ÷
           modifiers of the finding: Feen is the segment of 6 starting
           with the leftmost modifier of the finding and consists of the
           remaining sentence.
 findingseg (S. Fseg, Bagseg) :-
     partition(S, Begpart, Restpart),
     (Begpart - [], Begseg = [];
      Restpart = [], Faeg = [], Begseg • S;
     rightlatmod(Begpart, Begseg, Modseg)),
     append (Modeeg, Restpart, Pseg).
 findingseg(_,[],_) :- 1.
 actionfindingseg(S, Faeg, Begsag):-
       partition(S, Begpart, Restpart),
     (Begpart = [], Begseg = [];
      Restpart = {], Feeg = [], Beegeg = S;
       reverse (Baypart, ReversedBefore),
           findsubstance(ReversedBefore, Rest),
           append (Substancepart, Rest, ReversedBefore),
           reverse (Substancepart, Leftpart),
         reverse (Rest, Begseg) .
       append(Leftpart,Restpart,Fseg)).
 actionfindingseg(_,{],_) :- |.
 findaubatance((], [)):- !,
 findsubstance([X Rest], Rest):-
       substance( , [x], ()), ...
 findsubstance([X Rest1], Rest):-
       findsubstance (Rest1, Rest).
 % partition(+S,-Begpart,-Restpart); partitions sentence
         S is initial
 v partition(+8, -Begpart, -Restpart): partitions sentence
         8 is initial sentence; Begpart is part of sentence before the
 ¥
. t
           finding Restpart is the rest of the sentence and starts with
 *
           the finding. If there are 2 consecutive findings
           the 1st one is considered a modifier
 partition([),[],(]) :- !.
 partition([X|Rest],(X|Begpart),Restpart] :-
     not(isfinding(X)), |, partition(Rest, Begpart, Restpart).
 partition([X,Y|Rest],[X],[Y|Rest]) :-
     isfinding(X), isfinding(Y), |.
 partition([X|Rest],[],[X[Rest]) :-
     isfinding(X), (.
 $ isfinding(+X): is true if X is a word or phrase whose semantic class
         is a finding or subtype of finding.
```

```
isfinding(X) :-
     foundword(X,Sem),
                       + semantic class of word
                        t is class a type of (inding, recommend, or technique
     subtype(_,[Sem]),
& semantic class which are types of relevant information
Bubtype(finding,Sem) :-
     intersect (Sem, [attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, promote,
      siqmal]).
% there is only one type of technique class
subtype (technique, Sem) . .
     member (technique, Sem) .
subtype(time,$em) :-
     intersect (Sem. [status, sstatus, change, tmper, vstatus] ).
findinginlist(Sem) :-
    intersect(Sem, [attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, gromote,
      signal]).
Y chkforpunct(+W,+Rest): is true if there should be no space after word W
& nothing left to write.
chkforpunct(W,[]) :-!.
t is true if there should be no space before word after current word
chkforpunct(_,(W|_)) :-
   ispunct(W).
* ispunct(+W) is true if W is a punctuation for sentence print out
a rightletmod(List, Firstpart, Modpart): Modpart begins with the first
    word in List which is a modifier; Pirstpart are the preceding words
right1stmod([],[],[]} :- 1.
* X is a modifier or finding; Beginning part is empty
rightlatmod([X|Rest],[],[X|Rest]) :-
   foundword(X,Sem,Target),
   (modifier(Sem); Sem = p, Target = [_,conn]; subtype(_,(Sem])}, :.
X is not a modifier or finding
rightletmod([X|Rest],[X|Firstpart],Modpart) :-
   rightlstmod(Rest,Firstpart,Modpart).
frame(Frame, Type, Value, Mode): creates a list Frame, whose 1st
       element is Type, 2nd element is Value, and 3rd is a list of
Ł
       modifier frames or is emtpy
& Case where modifier list is empty; Value should be atom except for
certain types;
frame((Type, Value), Type, Value, X) :-
    (X = \{\})/X = \{\{\}\}\}, atom(Value), !.
3 Special cases where value of type should be a list
frame([Type, [H[R]], Type, [H[R], X) :-
       (x = \{\}; x = (\{\}\}),
       oklist(Type), !.
% Mcdifier list is merged with list consisting of Type and Value
frame(Prame, Type, Value, Mods) :-
     atom(Value),
     append({Type, Value], Mods, Prame), !.
```

```
frame (Frame, Type, [H|R], Mods):-
      is list(R),
      append(R, Mods, NewMods),
      append([Type, R], NewMods, Frame), !.
 & Components of Frame
 frame([Type, Value | Mods], Type, Value, Mods) :- ].
 % Value of Type should not be a list; first slement of value is real value
 frame([Type, R. Rest], Type, [8 | Rest], []) :- i.
 $ Special cases where value of type should be a list
 frame([Type,[H]R]),Type,[H]R),[] :- $repeated from rule above
     oklist(Type), !.
 Y Value of Type should not be a list; first element of value is real value
 frame(Frame, Type, (H|Rest), Mods) :-
     mergemods (Rest, Mods, NewMods),
     append{[Type,H],NewMods,Frame).
 b mergemodinf(-F,+frame,+Mods): Frame is a type-value-mod frame; Mods
     is an additional set of modifiers for Frame; mergemodinf adds Mods
     to Frame, resulting in F.
 mergemodinf({],[],_):-).
 mergemodinf(F,[rel,X|Rest],Modrel):-
         mergemodia?(Pl, Rest, Modrel),
         append([rel,X),Fi,F),!.
mergemodinf (P, [F1, X | Modfin], Modrel):
         atom(f1), mergemods [Modrel, Modfin, Mod),
         append([F1,X],Mod,F),!.
mergemedinf[F,[H|R],Modrel):-
        mergemodinf(F1,K,Modrel),
         mergemodinf(F2,R,Modrel),
         append([F1], F2, F),
 * addmodstof(+Args,+Mods,-NewArgs) is true if Args is a list of formats,
 * Mods is a list of modifiers and NewArgs is a list of formate where Mods
 t has been added to modifier list of that format
 eddmodstof([],_,[]) :~ |,
                             & no more formate
 addmodatof[[format1|Rest],Mods,[F1|NewRest]) :-
        mergemodinf(Fl,Formati,Mods). * merge modifiers into lat format
        addmodstof(Rest, Mods, NewRest), I. tadd modifier to remaining
 % oklist(+Type): is true if Type can have a list as its value
oklist(unitval).
oklist[age].
cklist (measure) .
oklist(prev_timeunit).
oklist(future_exam).
* mergemods(+Mods1,+Mods2,-Mod): Model and Mods2 are a list of modifier lists
٠
        Mod is the merged list; some elements of Mods1 and Mods2 may be
*
        empty
mergemods([],M,M) :- !.
mergemods (M, [], M).
mergemods (Mods1, Mods2, Mod) :-
        delete(Modal,(),M1),
        delets(Mods2,[],M2).
        append(M1,M2,Mod).
% addmod(+Mod,+Modlist,-NewMod): NewMod is formed by including
        Mod into Modlist
addmod([], Mod, Mod) :- |.
```

```
acdmod (Mod, [], [Mod]) :- 1.
addmod(Mod, Modlist, NewMod) : .
   app nd([Mod], Modlist, NewMod).
% modlist(+ListofMods,-Mods): ListofMods is a list consisting of
    individual modifier frames, some of which may be empty
    Mods is formed as a list of non-empty modifiers
modlist([),[]) :- 1.
t ignore a modifier which is an empty list
modlist([[]]R], Mode) :-
    modlist(R, Mods), 1.
modlist([[H|R1]|R2],Mods) :-
    atom(H), 1,
    modlist (R2, Rmods),
    addmod([H|R1],Rmpds,Mods).
modlist([[H|R1)|R2], Mods) :-
    is_list(N), !, & is first element is a list
    modlist (R2, Rmode).
    mergemoda([H|R1], Rmods, Mods).
%bpframe: creates from for sequences of bodyloc/region/position
bpframe(F,[], Type,Bp1,Bp2) :- % no conj relation but more than 1 bodyloc
        frame(Bpl,BplType,BplVal,Ep1Mods). %contents of Bpl frame
        frame(Ep2.Bp2Type, Bp2Val, Bp2Mods), *contents of Bp2 frame
        ( {EplType = region; BplType = position).
         Bp2Type - bodyloc, % 'left lung', 'area of lung'
mergemods(Sp1Mods, Bp2Mods, BpMods), % % % region modifier
         frame (NewBp2Mods, Bp1Type, Bp1Val, SpMods), snew Bp1 frame w new mod
                                                 t main frame is bodyloc
         frame(F, Bp2Type, Bp2Val, [NewBp2Mods])
         SpiType = bodyloc, Bp2Type = bodyloc, Type = main, *Sp2 is main
         mergemods (Bp1Mode, Bp2Mode, BpMods), thew bodyloe modifier
         frame (NewBp2Mods, Ep1Type, Bp1Val, BpMods), % 'joint of shoulder'
                                                      t main bp frame is shoulder
         frame (F, Sp2Type, Bp2Val, [NewSp2Mods])
         mergemods (BplMods, Bp2Mods, BpMods).
         frame (NewBpiMods, Bp2Typs, Bp2Val, BpMods), & 'shoulder joint'
                                                      w main by frame is shoulder
         frame(F, BplType, BplVal, [NewBplMode])
        ), I.
opframe (F, Rel, _, Bp1, Bp2) :- * no conj relation but more than 1 bodyloc
        Rel = (rel,Conj|_), 8p2 \= [],
        mergemode ([Sp1], (Bp2), Conjargs),
        frame(F, rel,Conj,Conjarge).
getrelation (R, F1, F2, F) :-
        [F2 \= [],
            (F1 = [rel,Conj1]Rest1], R = [rel,Conj],
                                    {Conjl = '.'; Conjl = or; Conjl = and},
                                    (Conj - ','; Conj = or; Conj = and);
              Rest1 = [F1]},
            \{F2 = \{rel, Conj2 | Rest2\},
                                    (Conj2 = 1,1; Conj2 = or; Conj2 = and);
              Rest2 = [F2]
            %splice([R,Restl,Rest2].F);
             append([R,Rest1,Rest2],F);
          P2 = [], F = F1 ).
```

```
uptotal :-
   addstotal(X),
   X =< 50,
   NewX is X + 1,
   rstractall(addstotal(X)),
   assert(addstotal(NewX)), ).</pre>
```

Appendix F .

\$save ('a'}='AAAC'; \$Bave{'b'}='AAAG'; \$seve('c')='AAAT'; Seave{'d'}='AACC'; \$pave{'c'}='AACG'; \$save{'f'}='AACT'; \$#Ave{'g'}='AAGC'; \$save{'h'}='AAGG'; \$save('i'}-'AAGT'; \$save('j')='AATC'; \$5&ve('k')='AATG'/ feave{'l'}='AATT'; \$save{'m'}='ACAC'; \$save{ 'n' }- 'ACAG' ; \$save{'o'}='ACAT'; \$save{'p'}='ACCC': \$save{'q'}='ACCG'; \$save{'r'}-'ACCT'; \$save{'s'}='ACGC'; \$55.c{'c'}='ACGG'; \$mave{'u'}='ACGT'; \$save{'v'}='ACTC'; \$save{'w'}='ACTG'; \$save{'x'}='ACTT'; \$aave{'v'}='AGAG'; \$save{'z'}='AGAT'/ \$save{'0'}='AGCC'; \$save('1'}='AGCG'; \$eave('2'}='AGCT'; \$save{'3'}='AGGC'; \$eave{'4'}='AGGG'; \$8ave('5')='A007'; \$cave{'6'}-'AGTC'; \$eave{ '7'}='AGTG'; \$save{'8'}='AGTT'; Ssave{'9'}='ATRT'; \$mave{' '}='ATCC'; \$save{!}'}-'ATCC'; \$mave{ '{'}='ATCC'; \$68ve{';'}='ATCC'; 5save(':')='ATCC'; \$64ve{'"'}-'ATEC'; \$eave{'\''}='ATTC'; \$66Ve{'?'}='ATCC'; \$eave{'!']='ATCC'; \$save{'#'}='CCCG'; \$84ve{'\$'}='CCCT'; \$save{'^'}='CCGG'; \$save{'&')='CCGT'; \$save{ '*! } = 'CCTG'; \$save{'(')='ATCC'; \$Bave{'}'}='ATCC';

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```
$save{'_'}='CGCT';
$save{'-'}='ATCC';
$save{'+'}='CGGT';
$save{'='}='CGTG';
$save(')'}='CGTT';
$save('{')-'CTCT';
$save(',')*'ATCC';
$save('.')='ATCC';
$save('|')~'CTTG';
$save{'%'}-'CTTT';
$save{ '/' }='ATCC';
$save{'\\')='GGTT':
$save{'@'}='GTGT';
$save{ *\n'] = 'ATCC';
$ Bave { '<' } = 'GTTT';
$gave('>')='GTTT';
$save('-')='GTTT';
```

Appendix F

```
#1/usr/bin/perl
#Scan.pl : Scans blast output
#Author: Michael Krauthammer
#Copyright: c.1999. Columbia University
#Variables
#blast imput/file
$input file="genebank.result";
#program output
$output_file="match.txt";
Hopen datastream for file which contains blast output
    open (INPUT, '/storage/psi blast/MarkIt/programs/markIt.cesult');
while ($line=cINPUT>){
    if ($line=-/\>gi\|(\d*( (.*)\,(.*)\,(.*)/)(
   $target-$4;
   $gi =$1;
   $semantic_class=$3;
   if($line==/Length = (.*)/{{
   $lengthI=$1;
    if ($Lipe-\/Identities \- (\d*)\//|}
   $length actual=$1
   if ($line=-/Query: (\d*)/}{
   Gstart-$1:
    1
#print if Subj 1, sometimes match 2 or 3 line long
    if ($line=-/Sbjct: 1 /}{
   if (($length_actual/$length1) > .9){
$target,"|",$start,"|",$start+$length1,"|",$semantic class,"|",$gi,"\n";
ł
```

Appendix G

```
#1/usr/bin/perl
#nucleotide_text_pareer.pl
#Author: michael Krauthammer, c.1999 Columbia University
open (INPUT, $ARGV(0));
#read uncoded input text line by line (chop it)
$all='':
while ($line=<INPUT>)(
    $alle$all.$line;
open (INPUTII, '/storsge/psi-blast/MarkIt/programs/markItII result');
open (OUTPUT, '>result.txt');
ffirst part: check matches, store positions
while ($line=<INPUTII>){
($name, $start, $end, $semantic_class, $gi) = $lins = -/(.*)\| (.*)\| (.*)\| (.*)\| (.*)\| (.*)\|
#divide by 4 (4 letter code)
$start=($st#rt-1)/4;
$end=($end-1)/4;
#get aubstring
if ($start |= 0){
51etters=substr($all,$start-1,$end-$start+3)."|";
5letters = ' '.substr($all,0,$end+2}."|";
[$letter_beginning) = $letters==/{4.}/;
$letter end=aubatr($all,$and,1);
$1ctter endII=substr{$all.$end,2};
#ignore matches that are in the MIDDLE of sentences, allow plurals
$letter_beginning=-tr/[A-2]/[a-2]/;
$letter_end=-tr/(A-Z)/{a-z}/;
if ((|($letter_beginning==/[a-t]/)| && ({!($letter_end==/(a-z)/|} ||
($1etter_endII=-/s /))|{
#make sure only the first occurence is stored at this position
   if ($save($start}==''){
   $save($start)=$end.'|'.$semantic_class.'|'.$gi;
          foreach $key(keys(%save)){
   {$end [key] = $pave{ $key} = -/^(.*) \ ] /;
   if ($end_key>$end){
      if ($keyc$start){
          $save($start)='null',
   }
}
```

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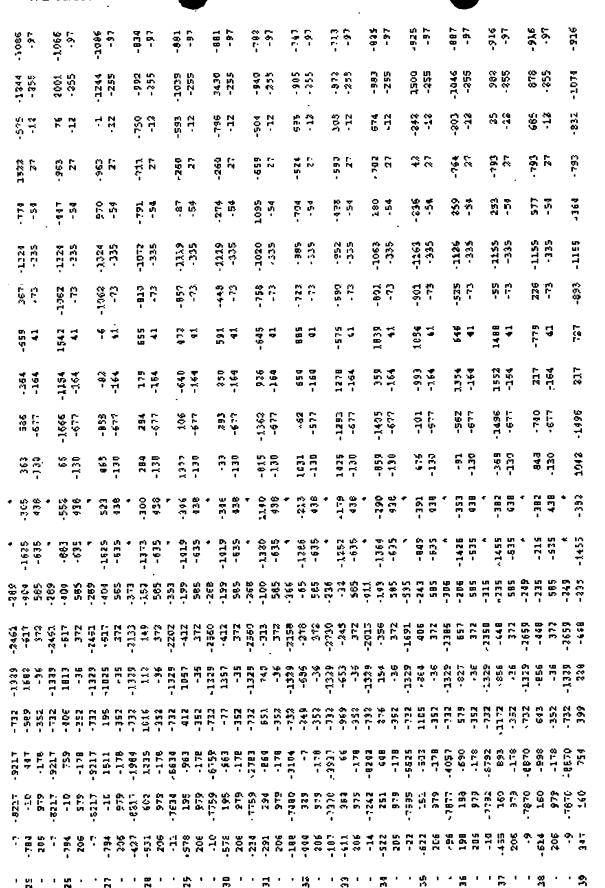
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